SEQUENCE LISTING

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(1) GENERAL INFORMATION:

- (i) APPLICANT: MAERTENS, GEERT
 BOSMAN, FONS
 DE MARTYNOFF, GUY
 BUYSE, MARIE-ANGE
- (ii) TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
- (iii) NUMBER OF SEQUENCES: 111
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON & VANDERHYE P.C.
 - (B) STREET: 1100 NORTH GLEBE ROAD
 - (C) CITY: ARLINGTON
 - (D) STATE: VIRGINIA
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 22201-4714
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/612,973
 - (B) FILING DATE: 11-MAR-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BYRNE, THOMAS E.
 - (B) REGISTRATION NUMBER: 32,205
 - (C) REFERENCE/DOCKET NUMBER: 1487-10
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 816-4000
 - (B) TELEFAX: (703) 816-4100
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

	Tyr	His	Val 35	Thr	Asn	Asp	Cys	Ser 40	Asn	Ser	Ser	Ile	Val 45	Tyr	Glu	Ala	
						CAC His											192
						TGC Cys 70											240
						CCC Pro											288
	Leu					GCT Ala											336
	TGC Cys	Gly	Ser 115	Val	Phe	CTC Leu	Val	Ser 120	Gln	Leu	Phe	Thr	Ile 125	Ser	Pro	Arg	384
	Arg	CAT His 130	GAG Glu	ACG Thr	GTG Val	CAG Gln	GAC Asp 135	TGC Cys	AAT Asn	TGC Cys	TCA Ser	ATC Ile 140	TAT Tyr	CCC Pro	GGC Gly	CAC His	432
	ATA Ile 145	ACA Thr	GGT Gly	CAC His	CGT Arg	ATG Met 150	GCT Ala	TGG Trp	GAT Asp	ATG Met	ATG Met 155	ATG Met	AAC Asn	TGG Trp	TCG Ser	CCT Pro 160	480
100	ACA Thr	ACG Thr	GCC Ala	CTG Leu	GTG Val 165	GTA Val	TCG Ser	CAG Gln	CTG Leu	CTC Leu 170	CGG Arg	ATC Ile	CCA Pro	CAA Gln	GCT Ala 175	GTC Val	528
						GGG Gly											576
						GGG Gly											624
		TTT Phe 210		CTC Leu	TAAT	rag											642
	(2)	INFO	ORMA:	rion	FOR	SEQ	ID N	10: 4	1:								
		{	(F	A) LE 3) TY	ENGTI (PE:	CHAE H: 21 amir DGY:	l2 an	mino cid									
		(ii)	MOI	LECUI	LE TY	YPE:	prot	ein									
		(xi)	SE	QUENC	CE DE	ESCRI	[PTIC	ON: S	SEQ :	D NO): 4:						
	Met 1	Pro	Gly	Cys	Ser 5	Phe	Ser	Ile	Phe	Leu 10	Leu	Ala	Leu	Leu	Ser 15	Cys	

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ille Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro ₌ 145 Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val 170 Twal Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala 180 Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu

200

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:

Leu Phe Ala Leu 210

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..792
- (ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
CACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
CTG LLeu 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TCC Ser																288
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TTG Leu	CTC Leu	GTT Val	GGG Gly 150	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys 155	TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val 160	480
GGG Gly	GAC Asp	CTC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528
TCG Ser	CCT Pro	CGC Arg	CGG Arg 180	CAT His	GAG Glu	ACG Thr	GTG Val	CAG Gln 185	GAC Asp	TGC Cys	AAT Asn	TGC Cys	TCA Ser 190	ATC Ile	TAT Tyr	576
CCC Pro	GGC Gly	CAC His 195	ATA Ile	ACG Thr	GGT Gly	CAC His	CGT Arg 200	ATG Met	GCT Ala	TGG Trp	GAT Asp	ATG Met 205	ATG Met	ATG Met	AAC Asn	624
TGG Trp	TCG Ser 210	CCT Pro	ACA Thr	ACG Thr	GCC Ala	CTG Leu 215	GTG Val	GTA Val	TCG Ser	CAG Gln	CTG Leu 220	CTC Leu	CGG Arg	ATC Ile	CCA Pro	672

CAA Gln 225	GCT Ala	GTC Val	GTG Val	GAC Asp	ATG Met 230	GTG Val	GCG Ala	GGG Gly	GCC Ala	CAT His 235	TGG Trp	GGA Gly	GTC Val	CTG Leu	GCG Ala 240	720
GGT Gly	CTC Leu	GCC Ala	TAC Tyr	TAT Tyr 245	TCC Ser	ATG Met	GTG Val	GGG Gly	AAC Asn 250	TGG Trp	GCT Ala	AAG Lys	GTT Val	TTG Leu 255	ATT Ile	768
	ATG Met						TAAT	rag								795
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	10: (5:								
	((E	A) LE 3) TY	NGTI PE:	CHAP H: 26 amir DGY:	33 ar	mino cid	rics: acid	: is							
and a	(ii)	MOI	LECUI	E T	YPE:	prot	cein									
	(xi)	SEC	QUENC	CE DI	ESCR	PTI	ои: :	SEQ :	ID NO): 6:						
Met 4 1	Leu	Gly	Lys	Val 5	Ile	Asp	Thr	Leu	Thr 10	Cys	Gly	Phe	Ala	Asp 15	Leu	
_ EVal	Gly	Tyr	Ile 20	Pro	Leu	Val	Gly	Ala 25	Pro	Leu	Gly	Gly	Ala 30	Ala	Arg	
Ala	Leu	Ala 35	His	Gly	Val	Arg	Val 40	Leu	Glu	Asp	Gly	Val 45	Asn	Tyr	Ala	
Thr	Gly 50	Asn	Leu	Pro	Gly	Cys 55	Ser	Phe	Ser	Ile	Phe 60	Leu	Leu	Ala	Leu	
Leu 65	Ser	Cys	Leu	Thr	Val 70	Pro	Ala	Ser	Ala	Tyr 75	Glu	Val	Arg	Asn	Val 80	
Ser	Gly	Met	Tyr	His 85	Val	Thr	Asn	Asp	Cys 90	Ser	Asn	Ser	Ser	Ile 95	Val	
Tyr	Glu	Ala	Ala 100	Asp	Met	Ile	Met	His 105		Pro	Gly	Cys	Val 110	Pro	Cys	
Val	Arg	Glu 115	Asn	Asn	Ser	Ser	Arg 120		Trp	Val	Ala	Leu 125	Thr	Pro	Thr	
Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135		Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His	
Val 145	Asp	Leu	Leu	Val	Gly 150	Ala	Ala	Ala	Phe	Cys 155	Ser	Ala	Met	Tyr	Val 160	
Gly	Asp	Leu	Cys	Gly 165		Val	Phe	Leu	Val 170		Gln	Leu	Phe	Thr 175	Ile	
Ser	Pro	Arg	Arg 180	His	Glu	Thr	Val	Gln 185		Cys	Asn	Cys	Ser 190	Ile	Tyr	

Pro	Gly	His 195	Ile	Thr	Gly	His	Arg 200	Met	Ala	Trp	Asp	Met 205	Met	Met	Asn	
Trp	Ser 210	Pro	Thr	Thr	Ala	Leu 215	Val	Val	Ser	Gln	Leu 220	Leu	Arg	Ile	Pro	
Gln 225	Ala	Val	Val	Asp	Met 230	Val	Ala	Gly	Ala	His 235	Trp	Gly	Val	Leu	Ala 240	
Gly	Leu	Ala	Tyr	Tyr 245	Ser	Met	Val	Gly	Asn 250	Trp	Ala	Lys	Val	Leu 255	Ile	
Val	Met	Leu	Leu 260	Phe	Ala	Pro										
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	10: 1	7:								
	(i)	(E		NGTH PE: RANI	H: 63 nucl DEDNE	3 ba .eic :SS:	ase pacionsing	pairs i	3							
	(ii)	MOI	LECUI	LE TY	YPE:	CDNA	A									
	(iii)	HYE	POTHE	ETICA	AL: 1	10										
	(iii)	ANT	rı-se	ENSE:	: NO											
	(ix)		ATURE A) NA B) LO	AME/E			530									
	(ix)		ATURE A) NA B) LO	AME/				tide								
	(xi)	SE(QUENC	CE DI	ESCR:	[PTI	ON:	SEQ :	ID NO	o: 7	:					
ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACG Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
ATG Met	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala	CCC Pro	CTA Leu	GGG Gly	GGT Gly	GCT Ala 30	GCC Ala	AGA Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAA Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCT Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTA Leu	192
CTG Leu 65	Ser	TGT Cys	CTG Leu	ACC Thr	ATT Ile 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240

					GTC Val											288
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACT Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TTG Leu	CTC Leu	GTT Val	GGG Gly 150	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys 155	TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val 160	480
VEGG VEly	GAT Asp	CTC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528
TCG Ser																576
CCC Pro	GGC Gly	CAC His 195	ATA Ile	ACA Thr	GGT Gly	CAC His	CGT Arg 200	ATG Met	GCT Ala	TGG Trp	GAT Asp	ATG Met 205	ATG Met	ATG Met	AAC Asn	624
TrgG Trp	TAA:	FAG														633

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1 5 10 15

Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 60

Leu 65	Ser	Cys	Leu	Thr	Ile 70	Pro	Ala	Ser	Ala	Tyr 75	Glu	Val	Arg	Asn	Val 80	
Ser	Gly	Met	Tyr	His 85	Val	Thr	Asn	Asp	Cys 90	Ser	Asn	Ser	Ser	Ile 95	Val	
Tyr	Glu	Ala	Ala 100	Asp	Met	Ile	Met	His 105	Thr	Pro	Gly	Cys	Val 110	Pro	Cys	
Val	Arg	Glu 115	Asn	Asn	Ser	Ser	Arg 120	Cys	Trp	Val	Ala	Leu 125	Thr	Pro	Thr	
Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135	Val	Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His	
Val 145	Asp	Leu	Leu	Val	Gly 150	Ala	Ala	Ala	Phe	Cys 155	Ser	Ala	Met	Tyr	Val 160	
EGly	Asp	Leu	Cys	Gly 165	Ser	Val	Phe	Leu	Val 170	Ser	Gln	Leu	Phe	Thr 175	Ile	
Ser	Pro	Arg	Arg 180	His	Glu	Thr	Val	Gln 185	Asp	Cys	Asn	Cys	Ser 190	Ile	Tyr	
EPro	Gly	His 195	Ile	Thr	Gly	His	Arg 200	Met	Ala	Trp	Asp	Met 205	Met	Met	Asn	
Trp																
$\mathbf{T}^{(2)}$	INF	ORMA!	rion	FOR	SEQ	ID 1	: OV	9:								
2000 2000 2000 2000 2000 2000 2000 200	(i)	(1	A) L: B) T' C) S'	ENGT: YPE: TRAN	HARAC H: 48 nuc DEDNI OGY:	33 b leic ESS:	ase pacions acions	pair: d	s							
	(ii) MO	LECU:	LE T	YPE:	cDN.	A									
	(iii) HY	POTH	ETIC.	AL:	NO										
	(iii) AN'	TI-S	ENSE	: NO											
	(ix	()		AME/	KEY:											
	(ix	()		AME/	KEY: ION:			tide								
	(xi) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0: 9	:					
ATG Met 1	CCC Pro	GGT Gly	TGC Cys	TCT Ser 5	TTC Phe	TCT Ser	ATC Ile	TTC Phe	CTC Leu 10	Leu	GCC Ala	CTG Leu	CTG Leu	TCC Ser 15	Cys	48
CTG	ACC	ATA	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	96

Leu	Thr	Ile	Pro 20	Ala	Ser	Ala	Tyr	Glu 25	Val	Arg	Asn	Val	Ser 30	Gly	Val	
TAC Tyr	CAT His	GTC Val 35	ACG Thr	AAC Asn	GAC Asp	TGC Cys	TCC Ser 40	AAC Asn	TCA Ser	AGC Ser	ATA Ile	GTG Val 45	TAT Tyr	GAG Glu	GCA Ala	144
GCG Ala	GAC Asp 50	ATG Met	ATC Ile	ATG Met	CAC His	ACC Thr 55	CCC Pro	GGG Gly	TGC Cys	GTG Val	CCC Pro 60	TGC Cys	GTT Val	CGG Arg	GAG Glu	192
GGC Gly 65	AAC Asn	TCC Ser	TCC Ser	CGT Arg	TGC Cys 70	TGG Trp	GTG Val	GCG Ala	CTC Leu	ACT Thr 75	CCC Pro	ACG Thr	CTC Leu	GCG Ala	GCC Ala 80	240
AGG Arg	AAC Asn	GCC Ala	AGC Ser	GTC Val 85	CCC Pro	ACA Thr	ACG Thr	ACA Thr	ATA Ile 90	CGA Arg	CGC Arg	CAC His	GTC Val	GAT Asp 95	TTG Leu	288
ECTC Leu																336
TGC Cys	GGA Gly	TCT Ser 115	GTT Val	TTC Phe	CTT Leu	GTT Val	TCC Ser 120	CAG Gln	CTG Leu	TTC Phe	ACC Thr	TTC Phe 125	TCA Ser	CCT Pro	CGC Arg	384
= CGG EArg	CAT His 130	CAA Gln	ACA Thr	GTA Val	CAG Gln	GAC Asp 135	TGC Cys	AAC Asn	TGC Cys	TCA Ser	ATC Ile 140	TAT Tyr	CCC Pro	GGC Gly	CAT His	432
GTA Val 145	TCA Ser	GGT Gly	CAC His	CGC Arg	ATG Met 150	GCT Ala	TGG Trp	GAT Asp	ATG Met	ATG Met 155	ATG Met	AAC Asn	TGG Trp	TCC Ser	TAATAG 160	483
(2)	INF	ORMA	rion	FOR	SEQ	ID	NO:	10:								
		(<u>)</u> (<u>1</u>	A) L: B) T'	ENGT YPE:	CHAI H: 1: amin OGY:	59 ai no a	mino cid									
	(ii) MO	LECU:	LE T	YPE:	pro	tein									
	(xi) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0: 1	0:					

- Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val 20 Z5 30 Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala 35
- Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu 50 60

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys 1 5 10 15

Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala 65 70 75 80

Arg	Asn	Ala	Ser	Val 85	Pro	Thr	Thr	Thr	Ile 90	Arg	Arg	His	Val	Asp 95	Leu		
Leu	Val	Gly	Ala 100	Ala	Ala	Phe	Cys	Ser 105	Ala	Met	Tyr	Val	Gly 110	Asp	Leu		
Cys	Gly	Ser 115	Val	Phe	Leu	Val	Ser 120	Gln	Leu	Phe	Thr	Phe 125	Ser	Pro	Arg		
Arg	His 130	Gln	Thr	Val	Gln	Asp 135	Cys	Asn	Cys	Ser	Ile 140	Tyr	Pro	Gly	His		
Val 145	Ser	Gly	His	Arg	Met 150	Ala	Trp	Asp	Met	Met 155	Met	Asn	Trp	Ser			
_ (2) 		ORMAT	QUEN	CE C	iara(CTER	ISTIC	CS:	_								
		(E	3) T C) S	ENGTH YPE: TRANI DPOLO	nuc! EDNI	leic ESS:	acio sino		5								
	(ii)	MOI	LECU	LE T	PE:	CDN2	F										
	(iii)	HY!	POTH	ETICA	AL: 1	NO.											
	(iii)) ANT	rı-sı	ENSE	: NO												
	(ix)		A) N	E: AME/I OCATI			477										
	(ix)		A) N.	E: AME/I OCATI				tide									
	(xi) SE	QUEN	CE DI	ESCR	IPTI	ON:	SEQ :	ID N	o: 1	1:						
ATG Met 1	TCC Ser	GGT Gly	TGC Cys	TCT Ser 5	TTC Phe	TCT Ser	ATC Ile	TTC Phe	CTC Leu 10	TTG Leu	GCC Ala	CTG Leu	CTG Leu	TCC Ser 15	TGT Cys		48
CTG Leu	ACC Thr	ATA Ile	CCA Pro 20	GCT Ala	TCC Ser	GCT Ala	TAT Tyr	GAA Glu 25	GTG Val	CGC Arg	AAC Asn	GTG Val	TCC Ser 30	GGG Gly	GTG Val		96
TAC Tyr	CAT His	GTC Val 35	ACG	AAC Asn	GAC Asp	TGC Cys	TCC Ser 40		TCA Ser	AGC Ser	ATA Ile	GTG Val 45	TAT	GAG Glu	GCA Ala	1	44
GCG Ala	GAC Asp 50	Met	ATC Ile	ATG Met	CAC His	ACC Thr 55	Pro	GGG Gly	TGC Cys	GTG Val	CCC Pro 60	TGC Cys	GTT Val	CGG Arg	GAG Glu	1	L92
GGC Gly 65	Asn	TCC Ser	TCC Ser	CGT Arg	TGC Cys 70	Trp	GTG Val	GCG Ala	CTC Leu	ACT Thr 75	Pro	ACG Thr	CTC Leu	GCG Ala	GCC Ala 80	2	240

AGG Arg	AAC Asn	GCC Ala	AGC Ser	GTC Val 85	CCC Pro	ACA Thr	ACG Thr	ACA Thr	ATA Ile 90	CGA Arg	CGC Arg	CAC His	GTC Val	GAT Asp 95	TTG Leu	288
CTC Leu	GTT Val	GGG Gly	GCT Ala 100	GCT Ala	GCT Ala	TTC Phe	TGT Cys	TCC Ser 105	GCT Ala	ATG Met	TAC Tyr	GTG Val	GGG Gly 110	GAT Asp	CTC Leu	336
TGC Cys	GGA Gly	TCT Ser 115	GTT Val	TTC Phe	CTT Leu	GTT Val	TCC Ser 120	CAG Gln	CTG Leu	TTC Phe	ACC Thr	ITC Phe 125	TCA Ser	CCT Pro	CGC Arg	384
Arg	His 130	Gln	Thr	Val	Gln	Asp 135	Cys	AAC Asn	Cys	Ser	Ile 140	Tyr	Pro	Gly	His	432
-GTA Val 145	TCA Ser	GGT Gly	CAC His	CGC Arg	ATG Met 150	GCT Ala	TGG Trp	GAT Asp	ATG Met	ATG Met 155	ATG Met	AAC Asn	TGG Trp	TAAT	'AG	480
⊈ ⊈(2)	INFO	ORMAT	rion	FOR	SEQ	ID 3	10: 3	12:								
		(<i>I</i> (I	A) LI B) T' O) T(ENGTI YPE: OPOLO	H: 15 amir DGY:	58 ar no ac line	mino cid ear	TICS: acid	: is							
i.	(ii)	MO]	LECU!	LE T	YPE:	prot	cein									
Spran :											,					
								SEQ :							~	
Met												Leu	Leu	Ser 15	Cys	
Met Met	Ser	Gly	Cys	Ser 5	Phe	Ser	Ile		Leu 10	Leu	Ala					
Met 1 Leu	Ser Thr	Gly	Cys Pro 20	Ser 5 Ala	Phe	Ser	Ile	Phe Glu	Leu 10 Val	Leu Arg	Ala Asn	Val	Ser 30	Gly	Val	
Met 1 Leu Tyr	Ser Thr His	Gly Ile Val 35	Cys Pro 20 Thr	Ser 5 Ala Asn	Phe Ser Asp	Ser Ala Cys	Ile Tyr Ser 40	Phe Glu 25	Leu 10 Val Ser	Leu Arg Ser	Ala Asn Ile	Val Val 45	Ser 30 Tyr	Gly Glu	Val Ala	
Met 1 Leu Tyr	Ser Thr His	Gly Ile Val 35	Cys Pro 20 Thr	Ser 5 Ala Asn Met	Phe Ser Asp	Ser Ala Cys Thr	Ile Tyr Ser 40 Pro	Phe Glu 25 Asn	Leu 10 Val Ser	Leu Arg Ser Val	Ala Asn Ile Pro 60	Val Val 45 Cys	Ser 30 Tyr Val	Gly Glu Arg	Val Ala Glu	
Met 1 Leu Tyr Ala Gly 65	Ser Thr His Asp 50 Asn	Gly Ile Val 35 Met Ser	Pro 20 Thr Ile Ser	Ser 5 Ala Asn Met Arg	Phe Ser Asp His Cys 70	Ser Ala Cys Thr 55	Tyr Ser 40 Pro	Phe Glu 25 Asn Gly	Leu 10 Val Ser Cys Leu	Leu Arg Ser Val Thr	Ala Asn Ile Pro 60 Pro	Val Val 45 Cys Thr	Ser 30 Tyr Val Leu	Gly Glu Arg Ala	Val Ala Glu Ala 80	
Met 1 Leu Tyr Ala Gly 65 Arg	Ser Thr His Asp 50 Asn	Gly Ile Val 35 Met Ser Ala	Pro 20 Thr Ile Ser	Ser 5 Ala Asn Met Arg Val 85	Phe Ser Asp His Cys 70 Pro	Ser Ala Cys Thr 55 Trp	Tyr Ser 40 Pro Val	Glu 25 Asn Gly Ala	Leu 10 Val Ser Cys Leu Ile 90	Leu Arg Ser Val Thr 75	Ala Asn Ile Pro 60 Pro Arg	Val Val 45 Cys Thr	Ser 30 Tyr Val Leu Val	Gly Glu Arg Ala Asp	Val Ala Glu Ala 80 Leu	
Met 1 Leu Tyr Ala Gly 65 Arg Leu	Ser Thr His Asp 50 Asn Asn	Gly Ile Val 35 Met Ser Ala Gly	Pro 20 Thr Ile Ser Ser Ala 100 Val	Ser 5 Ala Asn Met Arg Val 85 Ala	Phe Ser Asp His Cys 70 Pro	Ser Ala Cys Thr 55 Trp Thr	Ile Tyr Ser 40 Pro Val Thr	Glu 25 Asn Gly Ala Thr Ser 105 Gln	Leu 10 Val Ser Cys Leu Ile 90 Ala	Leu Arg Ser Val Thr 75 Arg	Ala Asn Ile Pro 60 Pro Arg	Val Val 45 Cys Thr His	Ser 30 Tyr Val Leu Val Gly 110	Gly Glu Arg Ala Asp 95 Asp	Val Ala Glu Ala 80 Leu Leu	
Met 1 Leu Tyr Ala Gly 65 Arg Leu Cys	Ser Thr His Asp 50 Asn Val	Gly Ile Val 35 Met Ser Ala Gly Ser 115 Gln	Pro 20 Thr Ile Ser Ser Ala 100 Val	Ser 5 Ala Asn Met Arg Val 85 Ala Phe	Phe Ser Asp His Cys 70 Pro Ala Leu	Ser Ala Cys Thr 55 Trp Thr Phe Val	Ile Tyr Ser 40 Pro Val Thr Cys Ser 120 Cys	Glu 25 Asn Gly Ala Thr Ser 105 Gln	Leu 10 Val Ser Cys Leu Ile 90 Ala	Leu Arg Ser Val Thr 75 Arg Met	Ala Asn Ile Pro 60 Pro Arg Tyr	Val 45 Cys Thr His Val Phe 125	Ser 30 Tyr Val Leu Val Gly 110 Ser	Gly Glu Arg Ala Asp 95 Asp	Val Ala Glu Ala 80 Leu Leu Arg	

(2) I	NFO	RMAT	ION	FOR	SEQ	ID N	0: 1	3:								
		(i)	(A (B (C) LE) TY () ST	E CH NGTH PE: RAND	: 63 nucl EDNE	6 ba eic SS:	se p acid sing	airs l								
	((ii)	MOL	ECUL	E TY	PE:	cDNA										
	(i	ii)	HYP	OTHE	TICA	L: N	10										
	i)	Lii)	ANT	'I-SE	NSE:	NO											
	,	(ix)	(A		: ME/K CATI			i33									
		(ix)	(A		E: AME/K DCATI				ide								
		(xi)	SEÇ	QUENC	CE DE	SCRI	PTIC	N: S	SEQ I	D NC): 13	3:					
□AT \Me	'G (CTG Leu	GGT Gly	AAG Lys	GCC Ala 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACG Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
Ī ατ	G (GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GC Al	CC (CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAA Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
AC Th	A.(GGG Gly 50	AAT Asn	TTG Leu	CCT Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTA Leu	192
Le	rg eu 65	TCC Ser	TGT Cys	CTA Leu	ACC Thr	ATT Ile 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAC Tyr 75	GAG Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
T(Se	CC :	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
T.	AT Yr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
G". Va	TT al	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
																	430

CTC GCG GCT AGG AAC GCC AGC ATC CCC ACT ACA ACA ATA CGA CGC CAC

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Le	u Al 13	_	ala	Arg	Asn	Ala	Ser 135	Ile	Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His	
	l As											TCC Ser					480
GG Gl	G GA y As	T C p L	TC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528
TC Se	G CC r Pr	T C o A	GC Arg	CGG Arg 180	CAT His	GAG Glu	ACG Thr	GTG Val	CAG Gln 185	GAC Asp	TGC Cys	AAT Asn	TGC Cys	TCA Ser 190	ATC Ile	TAT Tyr	576
		у Н										GAT Asp					624
···:	G TA p Ty 21	r	'AAT	'AG													640
s. 2.) IN		.) S (A	EQUE	ENCE ENGTH	SEQ CHAF H: 21	RACTE	ERIST	rics								
	(;	÷١) TO	POLO	OGY:	line										
			MOL) TO	POLO		line	ein	SEQ I	ID NO	D: 1	4:					
ē:	(x	i)	MOI SEQ) TO LECUI	OPOLO	OGY: (PE: ESCR)	line prot	cein				4: Gly	Phe	Ala	Asp 15	Leu	
	(x t Le l	i) u G	MOL SEÇ	D) TO LECUI QUENO Lys	DPOLO LE TY CE DE Ala 5	OGY: PE: ESCRI Ile	line prot PTIC Asp	ein ON: S	Leu	Thr 10	Cys				15		
Me Va	(x t Le l l Gl	i) u G y T	MOI SEÇ Ely Tyr	Lys Lle 20	DPOLO LE TY CE DE Ala 5 Pro	OGY: YPE: ESCRI Ile Leu	line prot PTIC Asp Val	cein ON: S Thr Gly	Leu Ala 25	Thr 10 Pro	Cys Leu	Gly	Gly	Ala 30	15 Ala	Arg	
Me Va Al	(xt Let l Gl a Let r Gl	i) u G y T u A	MOI SEQ Sly Syr	D) TO LECUI QUENO Lys Ile 20	DPOLO LE TY CE DE Ala 5 Pro Gly	OGY: PE: ESCRI Ile Leu Val	line prot EPTIC Asp Val Arg	Thr Gly Val 40	Leu Ala 25 Leu	Thr 10 Pro	Cys Leu Asp	Gly	Gly Val 45	Ala 30 Asn	15 Ala Tyr	Arg Ala	
Me Va Al	(xt Let l Gl a Let r Gl 5	i) y T u A y A	MOI SEÇ Gly 'yr 'yr Ala 35	Lys Lys Lys Lys Lecui	DPOLO LE TY LE DE Ala 5 Pro Gly Pro	OGY: YPE: YPE: Leu Val Gly	line prot PTIC Asp Val Arg Cys 55	Thr Gly Val 40 Ser	Leu Ala 25 Leu Phe	Thr 10 Pro Glu Ser	Cys Leu Asp	Gly Gly Gly Phe	Gly Val 45 Leu	Ala 30 Asn Leu	15 Ala Tyr Ala	Arg Ala Leu	
Me Va Al Th	t Le 1 Gl a Le r Gl 5	i) u G y T u A o r C	MOI SEQ Gly Cyr Ala 35	D) TO LECUI QUENO Lys Ile 20 His Leu	DPOLO DPOLO LE TY CE DE Ala 5 Pro Gly Pro Thr	OGY: YPE: ESCRI Ile Leu Val Gly Ile 70	line prot PTIC Asp Val Arg Cys 55	Thr Gly Val 40 Ser	Leu Ala 25 Leu Phe	Thr 10 Pro Glu Ser	Cys Leu Asp Ile Tyr 75	Gly Gly Phe 60	Gly Val 45 Leu Val	Ala 30 Asn Leu Arg	15 Ala Tyr Ala Asn	Arg Ala Leu Val 80	
Mee Va Al The Lee 6	t Le 1 Gl a Le r Gl 5 u Se r Gl	i) u G y T u A y A o C	MOI SEQ Gly Cyr Ala 35 Asn	D) TO LECUI QUENO Lys Ile 20 His Leu Leu	POLO LE TY LE DE Ala 5 Pro Gly Pro Thr His 85	OGY: YPE: ESCRI Ile Leu Val Gly Ile 70 Val	line prot PTIC Asp Val Arg Cys 55 Pro Thr	Thr Gly Val 40 Ser Ala Asn	Leu Ala 25 Leu Phe Ser Asp	Thr 10 Pro Glu Ser Ala Cys 90	Cys Leu Asp Ile Tyr 75 Ser	Gly Gly Phe 60	Gly Val 45 Leu Val	Ala 30 Asn Leu Arg	15 Ala Tyr Ala Asn Ile 95	Arg Ala Leu Val 80 Val	
Mee Va Al The Lee 6	t Le l Gl a Le r Gl s u Se r Gl	i) u G y T u A y A r C	MOI SEQ Gly Cyr Ala 35 Asn Cys	D) TO LECUI QUENO Lys Ile 20 His Leu Leu Tyr	POLO DPOLO DPOLO DPOLO DPOLO DPOLO Ala 5 Pro Gly Pro Thr His 85 Asp	OGY: YPE: ESCRI Ile Leu Val Gly Ile 70 Val Met	line prot PTIC Asp Val Arg Cys 55 Pro Thr	Thr Gly Val 40 Ser Ala Asn	Leu Ala 25 Leu Phe Ser Asp His 105	Thr 10 Pro Glu Ser Ala Cys 90 Thr	Cys Leu Asp Ile Tyr 75 Ser Pro	Gly Gly Phe 60 Glu Asn	Gly Val 45 Leu Val Ser Cys	Ala 30 Asn Leu Arg Ser Val 110	15 Ala Tyr Ala Asn Ile 95 Pro	Arg Ala Leu Val 80 Val Cys	

		130					135					140					
	Val 145	Asp	Leu	Leu	Val	Gly 150	Ala	Ala	Ala	Phe	Cys 155	Ser	Ala	Met	Tyr	Val 160	
	Gly	Asp	Leu	Суѕ	Gly 165	Ser	Val	Phe	Leu	Val 170	Ser	Gln	Leu	Phe	Thr 175	Ile	
	Ser	Pro	Arg	Arg 180	His	Glu	Thr	Val	Gln 185	Asp	Cys	Asn	Cys	Ser 190	Ile	Tyr	
	Pro	Gly	His 195	Ile	Thr	Gly	His	Arg 200	Met	Ala	Trp	Asp	Met 205	Met	Met	Asn	
	Trp	Tyr 210															
	(2)	INFO	ORMA:	rion	FOR	SEQ	ID 1	: OP	15:								
		(i)	() ()	A) L1 3) T' C) S'	ENGTI YPE : IRANI	HARAC nucl DEDNI DGY:	6 bas leic ESS:	se pa acio sino	airs d								
il.		(ii)	MOI	LECUI	LE T	YPE:	cDN	P									
-	į	(iii)	HY	POTH	ETICA	AL: 1	ON										
		(iii)	AN'	rI-SI	ENSE	: NO											
		(xi)	SE	QUEN	CE DI	ESCR	IPTI	: : NC	SEQ :	ID NO	D: 1	5:					
	ATG	CCCG	GTT (GCTC	rttc:	rc T	ATCT	Γ									26
	(2)	INFO	ORMA:	rion	FOR	SEQ	ID I	NO:	16:								
	,	(i)	() ()	A) L1 B) T' C) S'	ENGTI YPE: IRANI	HARAC H: 2: nuc. DEDNI	6 ba: leic ESS:	se pacionsino	airs d								
		(ii)	MO	LECU:	LE T	YPE:	cDN	Ą									
		(iii)	HY	POTH	ETIC	AL: I	ON										
		(iii)	AN'	ri-si	ENSE	: NO											
		(xi)	SE	QUEN	CE DI	ESCR:	IPTI(ON:	SEQ :	ID N	D: 1	6:					
	ATG	TTGG	STA A	AGGT	CATC	GA T	ACCC'	Γ									26
	(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	NO:	17:								
		(i)	SE	OUEN	CE C	HARA	CTER	ISTI	CS:								

		(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: YES	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
CTA	TTAGG	AC CAGTTCATCA TCATATCCCA	30
<u>=</u> (2)	INFO	RMATION FOR SEQ ID NO: 18:	
I I I	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
Figure 1	(iii)	ANTI-SENSE: YES	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
	ATTACC.	AG TTCATCATCA TATCCCA	27
(2)	INFO	RMATION FOR SEQ ID NO: 19:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
		SEQUENCE DESCRIPTION: SEQ ID NO: 19:	36
		CC ACGTCGATTC CCAGCTGTTC ACCATC	36
(2) INFO	RMATION FOR SEQ ID NO: 20:	

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs

		(C) ST	RAND	EDNE	eic SS: line	sing										
(i	Li)	MOL	ECUL	E TY	PE:	CDNA											
(ii	Li)	HYP	OTHE	TICA	L: N	10											
(ii	Li)	ANT	I-SE	NSE:	YES	;											
(x	۲i)	SEQ	UENC	E DE	SCRI	PTIC	n: S	EQ I	D NC): 20):						
GATGGT	rga <i>i</i>	AC A	GCTG	GGAA	T CG	ACGI	GGCG	TCG	TAT							36	
(2) IN	NFOE	RMAT	'ION	FOR	SEQ	ID N	10: 2	1:									
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 723 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO																
	(iii) HYPOTHETICAL: NO																
<u>ii</u> • (ii	(iii) HYPOTHETICAL: NO																
C (ii	(III) RIPOTRETICAD. NO																
(ii																	
(i	ix)	(A	ATURE A) NA B) LO	ME/F	ŒY:	mat 17	pept 17	ide									
(2	xi)	SEÇ	QUENC	E DE	SCRI	PTIC	N: S	SEQ I	D NO): 21	L:						
ATG TI Met Le																48	
GTG GO Val Gl	GG ' Ly '	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96	
GCC CT Ala Le	IG (eu 2	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144	
ACA GO Thr Gl	GG A	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192	
CTG TO Leu Se 65	CC '	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240	

	TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288	3
	Tyr	Glu	Ala	Ala 100	Asp	Met	Ile	ATG Met	His 105	Thr	Pro	Gly	Cys	Val 110	Pro	Cys	336	5
	GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384	1
	CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432	2
	GTC Val 145	GAT Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	480)
I	CAG Gln	GAC Asp	TGC Cys	AAT Asn	TGC Cys 165	TCA Ser	ATC Ile	TAT Tyr	CCC Pro	GGC Gly 170	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His 175	CGT Arg	528	3
	ATG Met	GCT Ala	TGG Trp	GAT Asp 180	ATG Met	ATG Met	ATG Met	AAC Asn	TGG Trp 185	TCG Ser	CCT Pro	ACA Thr	ACG Thr	GCC Ala 190	CTG Leu	GTG Val	576	5
	Val	TCG Ser	CAG Gln 195	CTG Leu	CTC Leu	CGG Arg	ATC Ile	CCA Pro 200	CAA Gln	GCT Ala	GTC Val	GTG Val	GAC Asp 205	ATG Met	GTG Val	GCG Ala	624	4
	GGG Gly	GCC Ala 210	CAT His	TGG Trp	GGA Gly	GTC Val	CTG Leu 215	GCG Ala	GGT Gly	CTC Leu	GCC Ala	TAC Tyr 220	TAT Tyr	TCC Ser	ATG Met	GTG Val	672	2
	GGG Gly 225	AAC Asn	TGG Trp	GCT Ala	AAG Lys	GTT Val 230	TTG Leu	ATT Ile	GTG Val	ATG Met	CTA Leu 235	CTC	TTT Phe	GCT Ala	CCC Pro	TAATAG 240	72	23

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Arg 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 55 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 105 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Wal Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val **1145** Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg 170 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val 180 z Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val 210 Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro 230 <u>1</u> 225

- (2) INFORMATION FOR SEQ ID NO: 23:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..558
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..555
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu		48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg		96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	1	44
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	1	92
CTG Leu G 65	Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	2	40
I TCC I Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	2	88
TAI Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys		36
GTI Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	3	84
L CTC	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	4	32
GTC Val 145	GAT Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	4	80
CÁC Glr	GAC Asp	TGC Cys	AAT Asn	TGC Cys 165	TCA Ser	ATC Ile	TAT Tyr	CCC Pro	GGC Gly 170	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His 175	CGT Arg	5	28
	GCT Ala								TAA	TAG						5	61

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu

10

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Wal Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
130 135 140

E Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val 150

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg 170

_Met Ala Trp Asp Met Met Met Asn Trp 180

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..603
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..600
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
□Leu 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
TTAT	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
_Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
∏ ECTC ⊨Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	480
CAG	GAC	TGC Cys	AAT Asn	TGC Cys 165	TCA	ATC Ile	TAT Tyr	Pro	GGC Gly 170	His	ATA Ile	Thr	Gly	His	CGT Arg	528
ATG Met	GCT Ala	TGG Trp	GAT Asp 180	Met	ATG Met	ATG Met	AAC Asn	TGG Trp 185	Ser	CCT Pro	ACA Thr	ACG Thr	GCC Ala 190	Leu	GTG Val	576
			Leu			ATC			TAG							606

(2) INFORMATION FOR SEQ ID NO: 26:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Wval Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val 145 150 150 155

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
165 170 175

Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val 180 185 190

Val Ser Gln Leu Leu Arg Ile Leu 195 200

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

	, ,		-													
ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
I ACA I Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
CTG Leu 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	480
CAG Gln	GAC Asp	TGC Cys	AAT Asn	TGC Cys 165	TCA Ser	ATC Ile	TAT Tyr	CCC Pro	GGC Gly 170	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His 175	CGT Arg	528
ATG Met	GCT Ala	TGG Trp	GAT Asp 180	ATG Met	ATG Met	ATG Met	AAC Asn	TGG Trp 185	TCG Ser	CCT Pro	ACA Thr	ACG Thr	GCC Ala 190	CTG Leu	GTG Val	576
GTA Val	TCG Ser	CAG Gln 195	Leu	CTC Leu	CGG Arg	ATC Ile	GTG Val 200	ATC Ile	GAG Glu	GGC	AGA Arg	CAC His 205	His	CAC His	CAC His	624
	CAC His	TAA	TAG													636

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(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

 Met Leu Gly Lys
 Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 15

 Wal Gly Tyr
 Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 30

 Wal Gly Asa Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asa Tyr Ala 35

 Wal Ser Cys Leu Thr Val Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 60

 Wal Ass Cys Cys Car Phe Ser Ile Phe Leu Leu Ala Leu 60

 Wal Ass Cys Cys Car Phe Ser Ile Phe Leu Leu Ala Leu 60

 Wal Arg Ass Val Thr Ass Asp Cys Ser Ala Tyr Glu Val Arg Ass Val 70

 War Pro Gly Cys Ser Ala Tyr Glu Val Arg Ass Val 70

 War Pro Gly Val Arg Ass Nal Ass Cys Ser Ass Ser Ser Ile Val 80

 War Pro Gly Val Arg Ass Nal Ass Val Thr Ass Ass Cys Ser Ass Ser Ser Ile Val 90

 War Pro Cys 110

 War Arg Glu Ass Ass Ass Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Cys 110

 Val Arg Glu Ass Arg Ass Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His 130

 Val Ass Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val 145

 Gln Ass Cys Ass Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg 165

 Met Ala Trp Asp Met Met Met Ass Trp Ser Pro Thr Thr Thr Thr Thr Ala Leu Val

Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His 195 200 205

His His 210

(2) INFORMATION FOR SEQ ID NO: 29:

180

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 630 base pairs

	(iii)	HYF	OTHE	TICA	AL: N	10										
	(iii)	ANT	I-SE	NSE:	МО											
	(ix)) NA	ME/K		CDS	527									
	(ix)		A) NA	ME/k		mat_ 16		ide								
Market St.	(xi)	SEC	QUENC	CE DE	ESCRI	PTIC	N: S	SEQ I	D NO): 29):					
ATO	GGT Gly	AAG Lys	GTC Val	ATC Ile 5	GAT Asp	ACC Thr	CTT Leu	ACG Thr	TGC Cys 10	GGA Gly	TTC Phe	GCC Ala	GAT Asp	CTC Leu 15	ATG Met	48
GGG Gly	TAC Tyr	ATC Ile	CCG Pro 20	CTC Leu	GTC Val	GGC Gly	GCT Ala	CCC Pro 25	GTA Val	GGA Gly	GGC Gly	GTC Val	GCA Ala 30	AGA Arg	GCC Ala	96
CTI Lev	GCG Ala	CAT His 35	GGC Gly	GTG Val	AGG Arg	GCC Ala	CTT Leu 40	GAA Glu	GAC Asp	GGG Gly	ATA Ile	AAT Asn 45	TTC Phe	GCA Ala	ACA Thr	144
GGC Gly	AAT Asn 50	TTG Leu	CCC Pro	GGT Gly	TGC Cys	TCC Ser 55	TTT Phe	TCT Ser	ATT Ile	TTC Phe	CTT Leu 60	CTC Leu	GCT Ala	CTG Leu	TTC Phe	192
TCT Ser 65	TGC Cys	TTA Leu	ATT Ile	CAT His	CCA Pro 70	GCA Ala	GCT Ala	AGT Ser	CTA Leu	GAG Glu 75	TGG Trp	CGG Arg	AAT Asn	ACG Thr	TCT Ser 80	240
GG(Gl ₃	CTC Leu	TAT Tyr	GTC Val	CTT Leu 85	ACC Thr	AAC Asn	GAC Asp	TGT Cys	TCC Ser 90	AAT Asn	AGC Ser	AGT Ser	ATT Ile	GTG Val 95	TAC Tyr	288
GA(G GCC 1 Ala	GAT Asp	GAC Asp 100	GTT Val	ATT Ile	CTG Leu	CAC His	ACA Thr 105	CCC Pro	GGC Gly	TGC Cys	ATA Ile	CCT Pro 110	TGT Cys	GTC Val	336
CA(Gl:	G GAC n Asp	GGC Gly 115	AAT Asn	ACA Thr	TCC Ser	ACG Thr	TGC Cys 120	TGG Trp	ACC Thr	CCA Pro	GTG Val	ACA Thr 125	CCT Pro	ACA Thr	GTG Val	384
GC! Ala	A GTC a Val 130	AAG Lys	TAC Tyr	GTC Val	GGA Gly	GCA Ala 135	ACC Thr	ACC Thr	GCT Ala	TCG Ser	ATA Ile 140	CGC Arg	AGT Ser	CAT His	GTG Val	432
GA(Asi	CTA Leu	TTA Leu	GTG Val	GGC Gly	GCG Ala 150	Ala	ACG Thr	ATG Met	TGC Cys	TCT Ser 155	Ala	CTC Leu	TAC Tyr	GTG Val	GGT Gly 160	480

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

	GAC Asp	ATG Met	TGT Cys	GGG Gly	GCT Ala 165	GTC Val	TTC Phe	CTC Leu	GTG Val	GGA Gly 170	CAA Gln	GCC Ala	TTC Phe	ACG Thr	TTC Phe 175	AGA Arg	528
	CCT Pro	CGT Arg	CGC Arg	CAT His 180	CAA Gln	ACG Thr	GTC Val	CAG Gln	ACC Thr 185	TGT Cys	AAC Asn	TGC Cys	TCG Ser	CTG Leu 190	TAC Tyr	CCA Pro	576
	GGC Gly	CAT His	CTT Leu 195	TCA Ser	GGA Gly	CAT His	CGA Arg	ATG Met 200	GCT Ala	TGG Trp	GAT Asp	ATG Met	ATG Met 205	ATG Met	AAC Asn	TGG Trp	624
	TAAT	AG															634
			(i) S (1 (I	TION SEQUE A) LE B) TY	ENCE ENGTI YPE :	CHAN H: 20 ami:	RACTE 08 ar	ERIST mino cid	rics	: is							
				LECUI					250	FD 37). J	٦.					
				QUENC Val									Ala	Asp	Leu	Met	
in the second	1				5					10					15		
	-	Tyr	Ile	Pro 20	Leu	Val	Gly	Ala	Pro 25	Val	Gly	Gly	Val	Ala 30	Arg	Ala	
	Leu	Ala	His 35	Gly	Val	Arg	Ala	Leu 40	Glu	Asp	Gly	Ile	Asn 45	Phe	Ala	Thr	
	Gly	Asn 50		Pro	Gly	Cys	Ser 55	Phe	Ser	Ile	Phe	Leu 60	Leu	Ala	Leu	Phe	
	Ser 65	Cys	Leu	Ile	His	Pro 70		Ala	Ser	Leu	Glu 75	Trp	Arg	Asn	Thr	Ser 80	
	Gly	Leu	Tyr	Val	Leu 85	Thr	Asn	Asp	Cys	Ser 90		Ser	Ser	Ile	Val 95	Tyr	
	Glu	Ala	Asp	Asp	Val	Ile	Leu	His	Thr 105		Gly	Cys	Ile	Pro 110	Cys	Val	
	Gln	Asp	Gly 115	Asn	Thr	Ser	Thr	Cys 120		Thr	Pro	Val	Thr 125	Pro	Thr	Val	
	Ala	Val 130		Tyr	Val	Gly	Ala 135		Thr	Ala	Ser	Ile 140	Arg	Ser	His	Val	
	Asp 145		Leu	Val	Gly	Ala 150		Thr	Met	Cys	Ser 155	Ala	Leu	Tyr	Val	Gly 160	
	Asp	Met	Cys	Gly	Ala 165		Phe	Leu	ı Val	Gly 170	Gln	Ala	Phe	Thr	Phe 175	Arg	

Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro 185 Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 200 (2) INFORMATION FOR SEQ ID NO: 31: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid(C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..627
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LCCATION: 1..624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG Met 1	GGT Gly	AAG Lys	GTC Val	ATC Ile 5	GAT Asp	ACC Thr	CTA Leu	ACG Thr	TGC Cys 10	GGA Gly	TTC Phe	GCC Ala	GAT Asp	CTC Leu 15	ATG Met	48
GGG Gľy	TAT Tyr	ATC Ile	CCG Pro 20	CTC Leu	GTA Val	GGC Gly	GGC Gly	CCC Pro 25	ATT Ile	GGG Gly	GGC Gly	GTC Val	GCA Ala 30	AGG Arg	GCT Ala	96
CTC Leu	GCA Ala	CAC His 35	GGT Gly	GTG Val	AGG Arg	GTC Val	CTT Leu 40	GAG Glu	GAC Asp	GGG Gly	GTA Val	AAC Asn 45	TAT Tyr	GCA Ala	ACA Thr	144
GGG Gly	AAT Asn 50	TTA Leu	CCC Pro	GGT Gly	TGC Cys	TCT Ser 55	TTC Phe	TCT Ser	ATC Ile	TTT Phe	ATT Ile 60	CTT Leu	GCT Ala	CTT Leu	CTC Leu	192
TCG Ser 65	TGT Cys	CTG Leu	ACC Thr	GTT Val	CCG Pro 70	GCC Ala	TCT Ser	GCA Ala	GTT Val	CCC Pro 75	TAC Tyr	CGA Arg	AAT Asn	GCC Ala	TCT Ser 80	240
GGG 31y	ATT Ile	TAT Tyr	CAT His	GTT Val 85	ACC Thr	AAT Asn	GAT Asp	TGC Cys	CCA Pro 90	AAC Asn	TCT Ser	TCC Ser	ATA Ile	GTC Val 95	TAT Tyr	288
GAG	GCA	GAT	AAC	CTG	ATC	CTA	CAC	GCA	CCT	GGT	TGC	GTG	CCT	TGT	GTC	336

Glu	Ala	Asp	Asn 100	Leu	Ile	Leu	His	Ala 105	Pro	Gly	Cys	Val	Pro 110	Cys	Val	
ATG Met	ACA Thr	GGT Gly 115	AAT Asn	GTG Val	AGT Ser	AGA Arg	TGC Cys 120	TGG Trp	GTC Val	CAA Gln	ATT Ile	ACC Thr 125	CCT Pro	ACA Thr	CTG Leu	384
TCA Ser	GCC Ala 130	CCG Pro	AGC Ser	CTC Leu	GGA Gly	GCA Ala 135	GTC Val	ACG Thr	GCT Ala	CCT Pro	CTT Leu 140	CGG Arg	AGA Arg	GCC Ala	GTT Val	432
GAC Asp 145	TAC Tyr	CTA Leu	GCG Ala	GGA Gly	GGG Gly 150	GCT Ala	GCC Ala	CTC Leu	TGC Cys	TCC Ser 155	GCG Ala	TTA Leu	TAC Tyr	GTA Val	GGA Gly 160	480
Asp	Ala	Cys	GGG Gly	Ala 165	Leu	Phe	Leu	Val	Gly 170	Gln	Met	Phe	Thr	Tyr 175	Arg	528
CCT CCT Pro	CGC Arg	CAG Gln	CAC His 180	GCT Ala	ACG Thr	GTG Val	CAG Gln	AAC Asn 185	TGC Cys	AAC Asn	TGT Cys	TCC Ser	ATT Ile 190	TAC Tyr	AGT Ser	576
L GGC	CAT His	GTT Val 195	ACC Thr	GGC Gly	CAC His	CGG Arg	ATG Met 200	GCA Ala	TGG Trp	GAT Asp	ATG Met	ATG Met 205	ATG Met	AAC Asn	TGG Trp	624
TAA	ГАG															630
1																
1 [[[(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO: 3	32:								
		(i) (i)	TION SEQUI A) LI B) T	ENCE ENGT YPE:	CHA: H: 2: ami:	RACTI 08 ai	ERIS' mino cid	rics								
		(i) (SEQUI A) LI B) T'	ENCE ENGT YPE: OPOL	CHA H: 2 ami: OGY:	RACT 08 am no am lin	ERIS' mino cid ear	rics								
(2)	(ii (xi	(i) ; (; () () MO	SEQUI A) LI B) T D) T LECU	ENCE ENGT YPE: OPOL	CHA H: 2 ami OGY: YPE:	RACTION OF THE PROPERTY OF THE	ERIS' mino cid ear tein ON:	rics acid	is ID N							
(2)	(ii (xi Gly	(i) ; (; () () MO	SEQUI A) LI B) T' D) T(ENCE ENGT YPE: OPOL	CHA H: 2 ami OGY: YPE:	RACTION OF THE PROPERTY OF THE	ERIS' mino cid ear tein ON:	rics acid	is ID N			Ala	Asp	Leu 15	Met	
(2) L Met	(ii (xi Gly	(i) :	SEQUI A) LI B) T D) T LECU	ENCE ENGT YPE: OPOL LE T CE D	CHA H: 2' ami OGY: YPE: ESCR	RACT: 08 and and align pro 1PTI Thr	ERIS' mino cid ear tein ON:	TICS acid	ID No Cys 10	Gly	Phe			15		
Met Gly	(ii (xi Gly Tyr	(i) ; (i)	SEQUI A) LI B) T D) T LECU QUEN Val Pro 20	ENCE ENGT YPE: OPOL LE T CE D Ile 5	CHAH: 20 ami: OGY: YPE: ESCR Asp	RACT: 08 an no ac lin pro IPTI Thr	ERIS' mino cid ear tein ON: Leu Gly	SEQ Thr Pro 25	ID No Cys 10 Ile	Gly	Phe	·Val	Ala 30 Tyr	Arg	Ala	
Met Leu	(ii (xi Gly Tyr	(i) ; (i) (i) (i) (i) (i) (i) (i) MO) SE Lys Ile His 35 Leu	SEQUI A) LI B) T D) T LECU QUEN Val Pro 20	ENCE ENGT YPE: OPOL LE T CE D Ile 5 Leu Val	CHAH: 20 ami: OGY: YPE: YPE: Asp Val	RACT: 08 an no ac lin pro IPTI Thr Gly Val	ERIS' mino cid ear tein ON: Leu Gly Leu 40	FICS acio SEQ Thr Pro 25 Glu	ID No Cys 10 Ile Asp	Gly	Phe Gly Val	·Val Asn 45	Ala 30 Tyr	Arg Ala	Ala Thr	
Met Leu Gly	(ii (xi Gly Tyr Ala Asn 50 Cys	(i) ; (i)	SEQUIAN LIBO TO DO TO	ENCE ENGT YPE: OPOL LE T CE D Ile 5 Leu Val	CHAH: 20 ami: OGY: YPE: ESCR Asp Val Arg	RACT: 08 an no a lin pro IPTI Thr Gly Val Ser 55	ERIS' mino cid ear tein ON: Leu Gly Leu 40 Phe	SEQ Thr Pro 25 Glu Ser	ID No Cys 10 Ile Asp	Gly Gly Phe	Phe Gly Val Ile 60	·Val Asn 45 Leu	Ala 30 Tyr Ala	Arg Ala Leu	Ala Thr	

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Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val 135 Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly 150 Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg 170 Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 200 4 4 4 4 4 5 6 (2) INFORMATION FOR SEQ ID NO: 33: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33: TGGGATATGA TGATGAACTG GTC

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(2) INFORMATION FOR SEQ ID NO: 34:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Q																
(2)	INFO	RMAT	rion	FOR	SEQ	ID N	10: 3	35:								
	(i)	(<i>I</i> (E	QUENC A) LE B) T) C) S1 O) TO	ENGTH (PE: [RANI	H: 14 nucl	176 k Leic ESS:	ase acio sino	pain i	cs							
	(ii)	MOI	LECUI	LE TY	PE:	CDNA	Ą									
	(iii)	HYE	POTHE	ETICA	AL: N	10										
	(iii)	ANT	rı-sı	ENSE:	: NO											
	(ix)	(<i>I</i>	ATURE A) NA B) LO	AME/E			L473									
		(Z (E	ATURI A) NA B) LO	AME/E	ON:	1	470									
=	(xi)	SE	QUENC	CE DE	ESCRI	IPTIC	ON: S	SEQ I	ID NO): 35	5:					
TrgG Trp 1	GAT Asp	ATG Met	ATG Met	ATG Met 5	AAC Asn	TGG Trp	TCG Ser	CCT Pro	ACA Thr 10	ACG Thr	GCC Ala	CTG Leu	GTG Val	GTA Val 15	TCG Ser	48
CAG	CTG Leu															96
	TGG Trp	Gly					Leu									144
	GCT Ala 50											GGC				192
	ACC Thr															240
	TCC Ser															288
	AAC Asn															336
	CTC Leu															384
AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	432

CTATTATGGT GGTAAGCCAC AGAGCAGGAG

Asn	Ser 130	Ser	Gly	Cys	Pro	Glu 135	Arg	Leu	Ala	Ser	Cys 140	Arg	Ser	Ile	Asp	
								CTC Leu								480
								CAC His								528
								GGT Gly 185								576
								GAT Asp								624
AAC Asn																672
CCG Pro 225																720
■TTC □Phe																768
AAC Asn								GAC Asp 265								816
FGCC Ala			GCC										CCT			864
ATG Met								TGG Trp								912
								TAC Tyr								960
								CGA Arg								1008
								CCG Pro 345								1056
								ACC Thr								1104
								ATC Ile								1152

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			TCG Ser													1200
			TTC Phe													1248
			CTG Leu 420													1296
			AAT Asn													1344
TTC Phe	CTT Leu 450	GTG Val	TTC Phe	TTC Phe	TGT Cys	GCT Ala 455	GCC Ala	TGG Trp	TAC Tyr	ATC Ile	AAG Lys 460	GGC Gly	AGG Arg	CTG Leu	GTC Val	1392
⊈CCT ⊈Pro <u>↓</u> 465																1440
CTG Leu										TAGT	ΓAA					1476
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	NO: 3	36:								
	((F	SEQUE A) LE B) TY	ENGT:	H: 49 amir	90 an 10 ac	nino cid									
AND THE STREET		(<i>I</i> (E ()	A) LE 3) TY	ENGTE (PE:)POL(H: 49 amir DGY:	90 am no ac line	nino cid ear									
AND THE STREET	(ii)	I) I) IOM	A) LE 3) TY 0) TO	ENGTH (PE:)POLO LE T	H: 49 amin DGY:	90 am no ac line prot	nino cid ear cein	acio	is): 3 (ā:					
	(ii) (xi)	(A (E (E MOI SEÇ	A) LE B) TY D) TO LECUI	ENGTH (PE: DPOLO LE TY	H: 49 amin DGY: (PE: ESCRI	90 am no ac line prot	nino cid ear ein	acio	is D NO			Leu	Val	Val 15	Ser	
Trp	(ii) (xi) Asp	(A (E (E MOI SEQ Met	A) LE B) TY D) TO LECUI	ENGTH (PE: OPOLO LE TY CE DE Met 5	H: 49 amir DGY: YPE: ESCRI	90 am no ac line prot PTIC	nino cid ear cein ON: S	acio	D NO	Thr	Ala			15		
Trp 1	(ii) (xi) Asp Leu	(A) (E) (E) MOI SEQ	A) LE B) TY C) TO LECUI QUENO Met Arg	ENGTH (PE:)POLO LE TY CE DE Met 5	H: 49 amir DGY: (PE: ESCRI Asn Pro	90 am no ac line prot PTIC Trp Gln	mino cid car cein ON: S Ser	SEQ 1 Pro Val 25	D NO Thr 10 Val	Thr Asp	Ala Met	Val	Ala 30	15 Gly	Ala	
Trp 1 Gln	(ii) (xi) Asp Leu Trp	MOI SEQ Met Leu Gly 35	A) LE B) TY D) TO LECUI QUENO Met Arg	ENGTH (PE:)POLO LE TY CE DE Met 5 Ile	H: 49 amir DGY: (PE: ESCRI Asn Pro	90 am no ac line prot PTIC Trp Gln Gly	aino cid ear cein ON: S Ser Ala Leu 40	SEQ Pro Val 25	Thr 10 Val	Thr Asp Tyr	Ala Met Ser	Val Met 45	Ala 30 Val	15 Gly Gly	Ala Asn	
Trp dl His	(ii) (xi) Asp Leu Trp Ala 50	MOI SEQ Met Leu Gly 35	A) LEGUI LECUI QUENC Met Arg 20 Val	ENGTH (PE: DPOLO LE TY CE DE Met 5 Ile Leu	H: 49 amir OGY: (PE: ESCRI Asn Pro Ala Val	90 am no ac line prot [PTIC Trp Gln Gly Val 55	nino cid ear cein ON: S Ser Ala Leu 40 Met	SEQ Pro Val 25 Ala Leu	Thr 10 Val	Thr Asp Tyr Phe	Ala Met Ser Ala 60	Val Met 45 Gly	Ala 30 Val	15 Gly Gly Asp	Ala Asn Gly	
Trp 1 Gln His Trp His 65	(ii) (xi) Asp Leu Trp Ala 50 Thr	MOI SEQ Met Leu Gly 35 Lys	A) LEGUI CUENC Met Arg 20 Val	ENGTH (PE: (PE) (POLO (PE) (POLO (PE) (PE) (PE) (PE) (PE) (PE) (PE) (PE)	H: 49 amir OGY: (PE: ESCRI Asn Pro Ala Val Gly 70	90 am no ac line prot PTIC Trp Gln Gly Val 55 Gly	nino cid ear cein ON: S Ser Ala Leu 40 Met	SEQ I Pro Val 25 Ala Leu	Thr 10 Val Tyr Leu Ala	Thr Asp Tyr Phe Ser 75	Ala Met Ser Ala 60 Asp	Val Met 45 Gly Thr	Ala 30 Val Val	15 Gly Gly Asp Gly	Ala Asn Gly Leu 80	

بالمصار المتنظي الخرار للمناصب والمراوية والمستخدم والمستحد والمستحد والمستحد والمستحد والمستحد والمستحد والمستحد

Ser	Leu	Gln 115	Thr	Gly	Phe	Phe	Ala 120	Ala	Leu	Phe	Tyr	Lys 125	His	Lys	Phe
Asn	Ser 130	Ser	Gly	Cys	Pro	Glu 135	Arg	Leu	Ala	Ser	Cys 140	Arg	Ser	Ile	Asp
Lys 145	Phe	Ala	Gln	Gly	Trp 150	Gly	Pro	Leu	Thr	Tyr 155	Thr	Glu	Pro	Asn	Ser 160
Ser	Asp	Gln	Arg	Pro 165	Tyr	Cys	Trp	His	Tyr 170	Ala	Pro	Arg	Pro	Cys 175	Gly
Ile	Val	Pro	Ala 180	Ser	Gln	Val	Cys	Gly 185	Pro	Val	Tyr	Cys	Phe 190	Thr	Pro
		Val 195					200	_				205			
E Asn	Trp 210	Gly	Ala	Asn	Asp	Ser 215	Asp	Val	Leu	Ile	Leu 220	Asn	Asn	Thr	Arg
© Pro	Pro	Arg	Gly	Asn	Trp 230	Phe	Gly	Cys	Thr	Trp 235	Met	Asn	Gly	Thr	Gly 240
Phe	Thr	Lys	Thr	Cys 245	Gly	Gly	Pro	Pro	Cys 250	Asn	Ile	Gly	Gly	Ala 255	Gly
= Asn	Asn	Thr	Leu 260	Thr	Cys	Pro	Thr	Asp 265	Cys	Phe	Arg	Lys	His 270	Pro	Glu
_Ala 		275			_		280					285		_	
■ Met ■	Val 290	His	Tyr	Pro	Tyr	Arg 295	Leu	Trp	His	Tyr	Pro 300	Cys	Thr	Val	Asn
Phe 305	Thr	Ile	Phe	Lys	Val 310	Arg	Met	Tyr	Val	Gly 315	Gly	Val	Glu	His	Arg 320
Phe	Glu	Ala	Ala	Cys 325	Asn	Trp	Thr	Arg	Gly 330	Glu	Arg	Cys	Asp	Leu 335	Glu
Asp	Arg	Asp	Arg 340	Ser	Glu	Leu	Ser	Pro 345	Leu	Leu	Leu	Ser	Thr 350	Thr	Glu
Trp	Gln	Ile 355	Leu	Pro	Cys	Ser	Phe 360	Thr	Thr	Leu	Pro	Ala 365	Leu	Ser	Thr
Gly	Leu 370	Ile	His	Leu	His	Gln 375	Asn	Ile	Val	Asp	Val 380	Gln	Tyr	Leu	Tyr
Gly 385	Val	Gly	Ser	Ala	Val 390	Val	Ser	Leu	Val	Ile 395	Lys	Trp	Glu	Tyr	Val 400
Leu	Leu	Leu	Phe	Leu 405	Leu	Leu	Ala	Asp	Ala 410	Arg	Ile	Cys	Ala	Cys 415	Leu
Trp	Met	Met	Leu 420	Leu	Ile	Ala	Gln	Ala 425	Glu	Ala	Ala	Leu	Glu 430	Asn	Leu
Val	Val	Leu	Asn	Ala	Ala	Ala	Val	Ala	Gly	Ala	His	Gly	Thr	Leu	Ser

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Pro Gly Ala Ala 465	a Tyr Ala Phe Tyr 470	Gly Val Trp Pro	Leu Leu Leu 480	
Leu Leu Ala Leu	u Pro Pro Arg Ala 485	Tyr Ala 490		
(2) INFORMATION	N FOR SEQ ID NO: 3	37:		
(A) I (B) T (C) S	NCE CHARACTERISTIC LENGTH: 1021 base TYPE: nucleic acid STRANDEDNESS: sind TOPOLOGY: linear	pairs i		
(ii) MOLEC	ULE TYPE: cDNA			
(iii) HYPOTH	HETICAL: NO			
(iii) ANTI-S	SENSE: NO			
	RE: NAME/KEY: CDS LOCATION: 21018			
	RE: NAME/KEY: mat_pept LOCATION: 21015	ide		
(xi) SEQUEN	NCE DESCRIPTION: S	SEQ ID NO: 37:		
	GCT GTC GTG GAC AT Ala Val Val Asp Me 5			46
	C CTC GCC TAC TAT y Leu Ala Tyr Tyr 20			94
	G ATG CTA CTC TTT l Met Leu Leu Phe 5			142
	G GCA GCA GCC TCC y Ala Ala Ala Ser 55			190
	G TCG GCT CAG AAA y Ser Ala Gln Lys 70		Asn Thr Asn Gly	238
	C AAC AGG ACT GCC a Asn Arg Thr Ala 85			286

440

Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val

	. GGG Gly															334	
	TGC Cys															382	
	GGG Gly															430	
	CCC Pro 145															478	
GCG Ala 160	TCT Ser	CAG Gln	GTG Val	TGC Cys	GGT Gly 165	CCA Pro	GTG Val	TAT Tyr	TGC Cys	TTC Phe 170	ACC Thr	CCG Pro	AGC Ser	CCT Pro	GTT Val 175	526	
GTG LVal	GTG Val	Gly	Thr	Thr 180	Asp	Arg	Phe	Gly	Val 185	Pro	Thr	Tyr	Asn	Trp 190	Gly	574	
GCG Ala	AAC Asn	GAC Asp	TCG Ser 195	GAT Asp	GTG Val	CTG Leu	ATT Ile	CTC Leu 200	AAC Asn	AAC Asn	ACG Thr	CGG Arg	CCG Pro 205	CCG Pro	CGA Arg	622	
E GGC	Asn	Trp 210	Phe	Gly	Cys	Thr	Trp 215	Met	Asn	Gly	Thr	Gly 220	Phe	Thr	Lys	670	
ACC Thr	TGT Cys 225	GGG Gly	GGC Gly	CCC Pro	CCG Pro	TGC Cys 230	AAC Asn	ATC Ile	GGG Gly	GGG Gly	GCC Ala 235	GGC Gly	AAC Asn	AAC Asn	ACC Thr	718	
	ACC Thr															766	
-	AGA Arg															814	
	CCA Pro															862	
	AAG Lys															910	
	TGC Cys 305															958	
	TCA Ser															1006	
GGC	AGA	GCT	TAAT	ATT												1021	

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Gly Arg Ala

- (2) INFORMATION FOR SEQ ID NO: 38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val L. Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe ■ Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly 100 Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg 130 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly 200 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu

Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala

235

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr 260 265 270	
Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe 275 280 285	
Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala 290 295 300	
Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg 305 310 315	
Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly 325 330 335	
Arg Ala	
(2) INFORMATION FOR SEQ ID NO: 39:	
(2) INFORMATION FOR SEQ ID NO: 39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1034 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (III) ANTI-SENSE: NO	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 21032	
<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 21029</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:	
G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly 1 5 10 15	46
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys 20 25 30	94
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg 35 40 45	142
GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu 50 55 60	190

	AGC Ser 65															238
	TGG Trp														CAA Gln 95	286
	GGG Gly															334
	TGC Cys															382
_Gln √		Trp 130	Gly	Pro	Leu	Thr	Tyr 135	Thr	Glu	Pro	Asn	Ser 140	Ser	Asp	Gln	430
LAGG LArg	CCC Pro 145	TAC Tyr	TGC Cys	TGG Trp	CAC His	TAC Tyr 150	GCG Ala	CCT Pro	CGA Arg	CCG Pro	TGT Cys 155	GGT Gly	ATT Ile	GTA Val	CCC Pro	478
GCG LAla 160																526
□GTG Val																574
GCG Ala	AAC Asn															622
	AAC Asn															670
	TGT Cys 225															718
Leu	ACC Thr				Asp					His					Tyr	766
	AGA Arg															814
	CCA Pro															862
	AAG Lys															910
	TGC Cys															958

305 310 315

AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG
Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Gly Asp Arg Gly
320 325 330 335

CAG ACA CCA TCA CCA TCA CTA AT AG

Gln Thr Pro Ser Pro Pro Ser Leu

340

- (2) INFORMATION FOR SEQ ID NO: 40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Tile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val

Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val

Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val

Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe
50 55 60

Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser 65 70 75 80

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr 85 90 95

Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly 100 105

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
115 120 125

Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg 130 135 140

Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala 145 150 155 160

Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val

Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala 180 185 190

Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly 195 200 205

Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala 250 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg **43**05 310 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln 325 Thr Pro Ser Pro Pro Ser Leu (2) INFORMATION FOR SEQ ID NO: 41: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 945 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..942 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 1..939 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41: ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT 96 Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp 25

ACC Thr	AGG Arg	GGC Gly 35	CTT Leu	GTG Val	TCC Ser	CTC Leu	TTT Phe 40	AGC Ser	CCC Pro	GGG Gly	TCG Ser	GCT Ala 45	CAG Gln	AAA Lys	ATC Ile	144
CAG Gln	CTC Leu 50	GTA Val	AAC Asn	ACC Thr	AAC Asn	GGC Gly 55	AGT Ser	TGG Trp	CAC His	ATC Ile	AAC Asn 60	AGG Arg	ACT Thr	GCC Ala	CTG Leu	192
AAC Asn 65	TGC Cys	AAC Asn	GAC Asp	TCC Ser	CTC Leu 70	CAA Gln	ACA Thr	GGG Gly	TTC Phe	TTT Phe 75	GCC Ala	GCA Ala	CTA Leu	TTC Phe	TAC Tyr 80	240
AAA Lys	CAC His	AAA Lys	TTC Phe	AAC Asn 85	TCG Ser	TCT Ser	GGA Gly	TGC Cys	CCA Pro 90	GAG Glu	CGC Arg	TTG Leu	GCC Ala	AGC Ser 95	TGT Cys	288
CGC Arg	TCC Ser	ATC Ile	GAC Asp 100	AAG Lys	TTC Phe	GCT Ala	CAG Gln	GGG Gly 105	TGG Trp	GGT Gly	CCC Pro	CTC Leu	ACT Thr 110	TAC Tyr	ACT Thr	336
IGAG IGlu I	CCT Pro	AAC Asn 115	AGC Ser	TCG Ser	GAC Asp	CAG Gln	AGG Arg 120	CCC Pro	TAC Tyr	TGC Cys	TGG Trp	CAC His 125	TAC Tyr	GCG Ala	CCT Pro	384
CGA Arg	CCG Pro 130	TGT Cys	GGT Gly	ATT Ile	GTA Val	CCC Pro 135	GCG Ala	TCT Ser	CAG Gln	GTG Val	TGC Cys 140	GGT Gly	CCA Pro	GTG Val	TAT Tyr	432
TGC Cys 145	TTC Phe	ACC Thr	CCG Pro	AGC Ser	CCT Pro 150	GTT Val	GTG Val	GTG Val	GGG Gly	ACG Thr 155	ACC Thr	GAT Asp	CGG Arg	TTT Phe	GGT Gly 160	480
¶GTC □Val □	CCC Pro	ACG Thr	TAT Tyr	AAC Asn 165	TGG Trp	GGG Gly	GCG Ala	AAC Asn	GAC Asp 170	TCG Ser	GAT Asp	GTG Val	CTG Leu	ATT Ile 175	CTC Leu	528
AAC Asn	AAC Asn	ACG Thr	CGG Arg 180	CCG Pro	CCG Pro	CGA Arg	GGC Gly	AAC Asn 185	TGG Trp	TTC Phe	GGC Gly	TGT Cys	ACA Thr 190	TGG Trp	ATG Met	576
AAT Asn	GGC Gly	ACT Thr 195	GGG Gly	TTC Phe	ACC Thr	AAG Lys	ACG Thr 200	TGT Cys	GGG Gly	GGC Gly	CCC Pro	CCG Pro 205	TGC Cys	AAC Asn	ATC Ile	624
GGG Gly	GGG Gly 210	GCC Ala	GGC Gly	AAC Asn	AAC Asn	ACC Thr 215	TTG Leu	ACC Thr	TGC Cys	CCC Pro	ACT Thr 220	GAC Asp	TGT Cys	TTT Phe	CGG Arg	672
AAG Lys 225	His	CCC Pro	GAG Glu	GCC Ala	ACC Thr 230	TAC Tyr	GCC Ala	AGA Arg	TGC Cys	GGT Gly 235	TCT Ser	GGG Gly	CCC Pro	TGG Trp	CTG Leu 240	720
ACA Thr	CCT Pro	AGG Arg	TGT Cys	ATG Met 245	GTT Val	CAT His	TAC Tyr	CCA Pro	TAT Tyr 250	AGG Arg	CTC Leu	TGG Trp	CAC His	TAC Tyr 255	CCC Pro	768
TGC Cys	ACT Thr	GTC Val	AAC Asn 260	TTC Phe	ACC Thr	ATC Ile	TTC Phe	AAG Lys 265	GTT Val	AGG Arg	ATG Met	TAC Tyr	GTG Val 270	GGG Gly	GGC Gly	816
GTG	GAG	CAC	AGG	TTC	GAA	GCC	GCA	TGC	AAT	TGG	ACT	CGA	GGA	GAG	CGT	864

Val	Glu	His	Arg	Phe	Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	Arg	
		275					280					285				
TGT Cys	GAC Asp 290	TTG Leu	GAG Glu	GAC Asp	AGG Arg	GAT Asp 295	AGA Arg	TCA Ser	GAG Glu	CTT Leu	AGC Ser 300	CCG Pro	CTG Leu	CTG Leu	CTG Leu	912
	ACA Thr									TAG						945
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	10: 4	12:								
	((E	A) LE 3) TY	NGTH	CHAF H: 31 amir OGY:	.4 am	ino id									
1000 E	(ii)	MOI	LECUI	E TY	PE:	prot	ein									
II I	(xi)	SEC	QUENC	CE DE	ESCRI	PTIC	N: S	SEQ I	ID NO): 42	2:					
Met 1	Val	Gly	Asn	Trp 5	Ala	Lys	Val	Leu	Val 10	Val	Met	Leu	Leu	Phe 15	Ala	
⊈Gly ≡	Val	Asp	Gly 20	His	Thr	Arg	Val	Ser 25	Gly	Gly	Ala	Ala	Ala 30	Ser	Asp	
Thr	Arg	Gly 35	Leu	Val	Ser	Leu	Phe 40	Ser	Pro	Gly	Ser	Ala 45	Gln	Lys	Ile	
∏ Gln	Leu 50	Val	Asn	Thr	Asn	Gly 55	Ser	Trp	His	Ile	Asn 60	Arg	Thr	Ala	Leu	
Asn 65	Cys	Asn	Asp	Ser	Leu 70	Gln	Thr	Gly	Phe	Phe 75	Ala	Ala	Leu	Phe	Tyr 80	
Lys	His	Lys	Phe	Asn 85	Ser	Ser	Gly	Cys	Pro 90	Glu	Arg	Leu	Ala	Ser 95	Cys	
Arg	Ser	Ile	Asp 100	Lys	Phe	Ala	Gln	Gly 105	Trp	Gly	Pro	Leu	Thr 110	Tyr	Thr	
Glu	Pro	Asn 115	Ser	Ser	Asp	Gln	Arg 120	Pro	Tyr	Cys	Trp	His 125	Tyr	Ala	Pro	
Arg	Pro 130	Cys	Gly	Ile	Val	Pro 135	Ala	Ser	Gln	Val	Cys 140	Gly	Pro	Val	Tyr	
Cys 145	Phe	Thr	Pro	Ser	Pro 150	Val	Val	Val	Gly	Thr 155	Thr	Asp	Arg	Phe	Gly 160	
Val	Pro	Thr	Tyr	Asn 165	Trp	Gly	Ala	Asn	Asp 170	Ser	Asp	Val	Leu	Ile 175	Leu	
Asn	Asn	Thr	Arg 180	Pro	Pro	Arg	Gly	Asn 185	Trp	Phe	Gly	Cys	Thr 190		Met	
Asn	Gly	Thr 195	Gly	Phe	Thr	Lys	Thr 200		Gly	Gly	Pro	Pro 205	Cys	Asn	Ile	

(Sly	Gly 210	Ala	Gly	Asn	Asn	Thr 215	Leu	Thr	Cys	Pro	Thr 220	Asp	Cys	Phe	Arg	
	Lys 225	His	Pro	Glu	Ala	Thr 230	Tyr	Ala	Arg	Cys	Gly 235	Ser	Gly	Pro	Trp	Leu 240	
7	Chr	Pro	Arg	Cys	Met 245	Val	His	Tyr	Pro	Tyr 250	Arg	Leu	Trp	His	Tyr 255	Pro	
(Cys	Thr	Val	Asn 260	Phe	Thr	Ile	Phe	Lys 265	Val	Arg	Met	Tyr	Val 270	Gly	Gly	
7	Val	Glu	His 275	Arg	Phe	Glu	Ala	Ala 280	Суѕ	Asn	Trp	Thr	Arg 285	Gly	Glu	Arg	
Ç.	Cys	Asp 290	Leu	Glu	Asp	Arg	Asp 295	Arg	Ser	Glu	Leu	Ser 300	Pro	Leu	Leu	Leu	
II II	Ser 305	Thr	Thr	Glu	Trp	Gln 310	Ser	Leu	Ile	Asn							
<u>1</u>	(2)				FOR												
		(i)	() () ()	A) Li B) T' C) S'	CE CI ENGTI YPE: TRANI OPOLO	H: 96 nucl DEDNI	61 ba Leic ESS:	ase p acid	pair: d	5							
E		(ii)	MO:	LECU:	LE T	YPE:	CDN	A									
		(iii)	HY	POTH	ETIC	AL: 1	10										
ļud.		(iii)) AN	ri-s	ENSE	: NO											
		(ix)		A) N	E: AME/! OCAT!			958									
	٠	(ix) FE. () ()	A) N.	E: AME/: OCAT	KEY: ION:	mat	_pep [.] 955	tide							•	
		(xi) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0: 4	3:					
	ATG Met 1	GTG Val	GGG Gly	AAC Asn	TGG Trp 5	GCT Ala	AAG Lys	GTT Val	TTG Leu	GTT Val 10	GTG Val	ATG Met	CTA Leu	CTC Leu	TTT Phe 15	GCC Ala	48
	GGC Gly	GTC Val	GAC Asp	GGG Gly 20	His	ACC Thr	CGC Arg	GTG Val	TCA Ser 25	GGA Gly	GGG Gly	GCA Ala	GCA Ala	GCC Ala 30	TCC Ser	GAT Asp	96
	ACC Thr	AGG Arg	GGC Gly 35	Leu	GTG Val	TCC Ser	CTC Leu	TTT Phe 40	Ser	CCC Pro	GGG Gly	TCG Ser	GCT Ala 45	Gln	AAA Lys	ATC Ile	144
	CAG	CTC	GTA	AAC	ACC	AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	CTG	192

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	Gln	Leu 50	Val	Asn	Thr	Asn	Gly 55	Ser	Trp	His	Ile	Asn 60	Arg	Thr	Ala	Leu	
									GGG Gly								240
									TGC Cys								288
									GGG Gly 105								336
united S	Glu								CCC Pro								384
	CGA Arg	CCG Pro 130	TGT Cys	GGT Gly	ATT Ile	GTA Val	CCC Pro 135	GCG Ala	TCT Ser	CAG Gln	GTG Val	TGC Cys 140	GGT Gly	CCA Pro	GTG Val	TAT Tyr	432
	Cys 145	TTC Phe	ACC Thr	CCG Pro	AGC Ser	CCT Pro 150	GTT Val	GTG Val	GTG Val	GGG Gly	ACG Thr 155	ACC Thr	GAT Asp	CGG Arg	TTT Phe	GGT Gly 160	480
10 10 10 10 10 10 10 10 10 10 10 10 10 1	CTC	CCC Pro	ACG Thr	TAT Tyr	AAC Asn 165	TGG Trp	GGG Gly	GCG Ala	AAC Asn	GAC Asp 170	TCG Ser	GAT Asp	GTG Val	CTG Leu	ATT Ile 175	CTC Leu	528
	Asn								AAC Asn 185								576
Start.									TGT Cys								624
									ACC Thr								672
									AGA Arg								720
	ACA Thr	CCT Pro	AGG Arg	TGT Cys	ATG Met 245	GTT Val	CAT His	TAC Tyr	CCA Pro	TAT Tyr 250	AGG Arg	CTC Leu	TGG Trp	CAC His	TAC Tyr 255	CCC Pro	768
									AAG Lys 265								816
									TGC Cys								864
									TCA Ser								912

300 290 295 TCT ACA ACA GGT GAT CGA GGG CAG ACA CCA TCA CCA TCA CTA A 958 Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu 310 305 961 TAG (2) INFORMATION FOR SEQ ID NO: 44: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44: Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys

Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr
100 105 110

Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro 115 120 125

Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr 130 135 140

Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly 145 150 155 160

Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu 165 170 175

Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met 180 185 190

Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile 195 200 205

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg 210 220

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu

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2	25					230					235					240	
T	hr	Pro	Arg	Cys	Met 245	Val	His	Tyr	Pro	Tyr 250	Arg	Leu	Trp	His	Tyr 255	Pro	
C	ys	Thr	Val	Asn 260	Phe	Thr	Ile	Phe	Lys 265	Val	Arg	Met	Tyr	Val 270	Gly	Gly	
V	al	Glu	His 275	Arg	Phe	Glu	Ala	Ala 280	Cys	Asn	Trp	Thr	Arg 285	Gly	Glu	Arg	
C	ys	Asp 290	Leu	Glu	Asp	Arg	Asp 295	Arg	Ser	Glu	Leu	Ser 300	Pro	Leu	Leu	Leu	
	er 05	Thr	Thr	Gly	Asp	Arg 310	Gly	Gln	Thr	Pro	Ser 315	Pro	Pro	Ser	Leu		
(2)	INFO	RMA	rion	FOR	SEQ	ID 1	NO: 4	15:								
		(i)	(<i>I</i> (E	A) LI B) T' C) S'	CE CH ENGTH YPE: TRANI OPOLO	H: 13 nucl DEDNE	395 k Leic ESS:	ase acio sino	pai:	rs							
		(ii)	MOI	LECUI	LE TY	YPE:	CDNA	j.									
		(iii)	HYE	POTH	ETICA	AL: 1	10										
	((iii)	ANT	rI-Si	ENSE	: NO											
		(ix)		A) N	E: AME/I DCATI			1392									
		(ix)		A) NA	E: AME/E CCATI		-		ide								
	•	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	on: s	SEQ 1	ED NO): 45	5:					
									GTC Val								48
									GTT Val 25								96
			Val						GTG Val								144
								CTC	TTT Phe				TCG				192
I.									AGT Ser								240

	AAC Asn															288
TAC Tyr	AAA Lys	CAC His	AAA Lys 100	TTC Phe	AAC Asn	TCG Ser	TCT Ser	GGA Gly 105	TGC Cys	CCA Pro	GAG Glu	CGC Arg	TTG Leu 110	GCC Ala	AGC Ser	336
TGT Cys	CGC Arg	TCC Ser 115	ATC Ile	GAC Asp	AAG Lys	TTC Phe	GCT Ala 120	CAG Gln	GGG Gly	TGG Trp	GGT Gly	CCC Pro 125	CTC Leu	ACT Thr	TAC Tyr	384
	GAG Glu 130															432
CCT Pro 145	CGA Arg	CCG Pro	TGT Cys	GGT Gly	ATT Ile 150	GTA Val	CCC Pro	GCG Ala	TCT Ser	CAG Gln 155	GTG Val	TGC Cys	GGT Gly	CCA Pro	GTG Val 160	480
TAT Tyr	TGC Cys	TTC Phe	ACC Thr	CCG Pro 165	AGC Ser	CCT Pro	GTT Val	GTG Val	GTG Val 170	GGG Gly	ACG Thr	ACC Thr	GAT Asp	CGG Arg 175	TTT Phe	528
GGT Gly	GTC Val	CCC Pro	ACG Thr 180	TAT Tyr	AAC Asn	TGG Trp	GGG Gly	GCG Ala 185	AAC Asn	GAC Asp	TCG Ser	GAT Asp	GTG Val 190	CTG Leu	ATT Ile	576
CTC Leu	AAC Asn	AAC Asn 195	ACG Thr	CGG Arg	CCG Pro	CCG Pro	CGA Arg 200	GGC Gly	AAC Asn	TGG Trp	TTC Phe	GGC Gly 205	TGT Cys	ACA Thr	TGG Trp	624
ATG Met																672
	GGG Gly															720
	AAG Lys															768
	ACA Thr															816
	TGC Cys		GTC					TTC					TAC			864
	GTG Val 290															912
	TGT Cys															960
CTG	TCT	ACA	ACA	GAG	TGG	CAG	ATA	CTG	CCC	TGT	TCC	TTC	ACC	ACC	CTG	1008

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Leu	Ser	Thr	Thr	Glu 325	Trp	Gln	Ile	Leu	Pro 330	Cys	Ser	Phe	Thr	Thr 335	Leu	
					GGC Gly											1056
GTG Val	CAA Gln	TAC Tyr 355	CTG Leu	TAC Tyr	GGT Gly	GTA Val	GGG Gly 360	TCG Ser	GCG Ala	GTT Val	GTC Val	TCC Ser 365	CTT Leu	GTC Val	ATC Ile	1104
					CTG Leu										CGC Arg	1152
ATC Ile 385	TGC Cys	GCC Ala	TGC Cys	TTA Leu	TGG Trp 390	ATG Met	ATG Met	CTG Leu	CTG Leu	ATA Ile 395	GCT Ala	CAA Gln	GCT Ala	GAG Glu	GCC Ala 400	1200
GCC TAla																1248
CAT His																1296
= AAG																1344
CCG TPro L															TAGTAA	1395
					-											

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr
1 10 15

Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe 20 25 30

Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser 35 40 45

Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys 50 55 60

Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala 65 70 75 80

Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala 130 Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe 165 Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile 185 teu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn
210
220 Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe 235 Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala

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Lys	Gly	Arg 435	Leu	Val	Pro	Gly	Ala 440	Ala	Tyr	Ala	Phe	Tyr 445	Gly	Val	Trp	
Pro	Leu 450	Leu	Leu	Leu	Leu	Leu 455	Ala	Leu	Pro	Pro	Arg 460	Ala	Tyr	Ala		
(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	10: 4	17:								
	(i)	() ()	A) L1 B) T1 C) S1	engti YPE : TRANI	i: 20 nucl	OTERI 082 h leic ESS: line	ase acio sino	pai: i	cs							
	(ii)	MOI	LECUI	LE T	YPE:	CDNA	A									
	(iii)	HYI	POTH:	ETICA	AL: 1	40										
	(iii)	ANT	ri-si	ENSE	: NO											
		(<i>)</i> (E FE <i>I</i>	3) LO ATURI	AME/E DCATE	ON:	CDS 12		ide								
		(E	3) L(DCAT I	ON:	$1\overline{2}$	2076									
	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	on: s	SEQ 1	D NO): 47	7:					
	(xi) TTG Leu	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACA	TGC	GGC					48
Asn 1 GTG	TTG	GGT Gly TAC	AAG Lys	GTC Val 5	ATC Ile	GAT Asp GTC	ACC Thr	CTT Leu GCC	ACA Thr 10	TGC Cys	GGC Gly GGG	Phe GGC	Ala GCT	Asp 15 GCC	Leu AGG	48 96
Asn 1 GTG Val	TTG Leu GGG	GGT Gly TAC Tyr	AAG Lys ATT Ile 20 CAT	GTC Val 5 CCG Pro	ATC Ile CTC Leu GTC	GAT Asp GTC Val	ACC Thr GGC Gly	CTT Leu GCC Ala 25	ACA Thr 10 CCC Pro	TGC Cys CTA Leu	GGC Gly GGG Gly	Phe GGC Gly GTG	Ala GCT Ala 30 AAC	Asp 15 GCC Ala TAT	Leu AGG Arg GCA	
Asn 1 GTG Val GCC Ala	TTG Leu GGG Gly	GGT Gly TAC Tyr GCG Ala 35	AAG Lys ATT Ile 20 CAT His	GTC Val 5 CCG Pro GGC Gly	ATC Ile CTC Leu GTC Val	GAT Asp GTC Val CGG Arg	ACC Thr GGC Gly GTT Val 40 TCT	CTT Leu GCC Ala 25 CTG Leu	ACA Thr 10 CCC Pro GAG Glu	TGC Cys CTA Leu GAC Asp	GGC Gly GGG Gly TTC	Phe GGC Gly GTG Val 45 CTC	Ala GCT Ala 30 AAC Asn	Asp 15 GCC Ala TAT Tyr	AGG Arg GCA Ala	96
Asn 1 GTG Val GCC Ala ACA Thr	TTG Leu GGG Gly CTG Leu GGG Gly	GGT Gly TAC Tyr GCG Ala 35 AAT Asn	AAG Lys ATT Ile 20 CAT His TTG Leu	GTC Val 5 CCG Pro GGC Gly CCC Pro	ATC Ile CTC Leu GTC Val GGT Gly GTT	GAT Asp GTC Val CGG Arg TGC Cys 55	ACC Thr GGC Gly GTT Val 40 TCT Ser GCT	CTT Leu GCC Ala 25 CTG Leu TTC Phe	ACA Thr 10 CCC Pro GAG Glu TCT Ser	TGC Cys CTA Leu GAC Asp ATC Ile	GGC Gly GGC Gly TTC Phe 60 GAA	GGC Gly GTG Val 45 CTC Leu GTG	GCT Ala 30 AAC Asn TTG Leu	Asp 15 GCC Ala TAT Tyr GCT Ala	AGG Arg GCA Ala TTG Leu GTG	96 144
Asn 1 GTG Val GCC Ala ACA Thr CTG Leu 65	TTG Leu GGG Gly CTG Leu GGG Gly 50	GGT Gly TAC Tyr GCG Ala 35 AAT Asn TGT Cys	AAG Lys ATT Ile 20 CAT His TTG Leu CTG Leu	GTC Val 5 CCG Pro GGC Gly CCC Pro ACC Thr	ATC Ile CTC Leu GTC Val GGT Gly GTT Val 70 GTC	GAT Asp GTC Val CGG Arg TGC Cys 55 CCA Pro	ACC Thr GGC Gly GTT Val 40 TCT Ser GCT Ala	CTT Leu GCC Ala 25 CTG Leu TTC Phe	ACA Thr 10 CCC Pro GAG Glu TCT Ser GCT Ala	TGC Cys CTA Leu GAC Asp ATC Ile TAT Tyr 75	GGC Gly GGC Gly TTC Phe 60 GAA Glu	Phe GGC Gly GTG Val 45 CTC Leu GTG Val	GCT Ala 30 AAC Asn TTG Leu CGC Arg	Asp 15 GCC Ala TAT Tyr GCT Ala AAC Asn	AGG Arg GCA Ala TTG Leu GTG Val 80 GTG	96 144 192

410

405

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TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TTG Leu	CTC Leu	GTT Val	GGG Gly 150	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys 155	TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val 160	480
Gly	GAC Asp	CTC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528
¶ ∏TCG ∏Ser	CCT Pro	CGC Arg	CGG Arg 180	CAT His	GAG Glu	ACG Thr	GTG Val	CAG Gln 185	GAC Asp	TGC Cys	AAT Asn	TGC Cys	TCA Ser 190	ATC Ile	TAT Tyr	576
LCCC LPro	GGC Gly	CAC His 195	ATA Ile	ACG Thr	GGT Gly	CAC His	CGT Arg 200	ATG Met	GCT Ala	TGG Trp	GAT Asp	ATG Met 205	ATG Met	ATG Met	AAC Asn	624
TGG Trp	TCG Ser 210	CCT Pro	ACA Thr	ACG Thr	GCC Ala	CTG Leu 215	GTG Val	GTA Val	TCG Ser	CAG Gln	CTG Leu 220	CTC Leu	CGG Arg	ATC Ile	CCA Pro	672
CAA Gln 225	GCT Ala	GTC Val	GTG Val	GAC Asp	ATG Met 230	GTG Val	GCG Ala	GGG Gly	GCC Ala	CAT His 235	TGG Trp	GGA Gly	GTC Val	CTG Leu	GCG Ala 240	720
GGC Gly	CTC Leu	GCC Ala	TAC Tyr	TAT Tyr 245	TCC Ser	ATG Met	GTG Val	GGG Gly	AAC Asn 250	TGG Trp	GCT Ala	AAG Lys	GTT Val	TTG Leu 255	GTT Val	768
GTG Vál	ATG Met	CTA Leu	CTC Leu 260	TTT Phe	GCC Ala	GGC Gly	GTC Val	GAC Asp 265	GGG Gly	CAT His	ACC Thr	CGC Arg	GTG Val 270	TCA Ser	GGA Gly	816
GGG Gly	GCA Ala	GCA Ala 275	GCC Ala	TCC Ser	GAT Asp	ACC Thr	AGG Arg 280	GGC Gly	CTT Leu	GTG Val	TCC Ser	CTC Leu 285	TTT Phe	AGC Ser	CCC Pro	864
GGG Gly	TCG Ser 290	GCT Ala	CAG Gln	AAA Lys	ATC Ile	CAG Gln 295	CTC Leu	GTA Val	AAC Asn	ACC Thr	AAC Asn 300	GGC Gly	AGT Ser	TGG Trp	CAC His	912
ATC Ile 305	AAC Asn	AGG Arg	ACT Thr	GCC Ala	CTG Leu 310	AAC Asn	TGC Cys	AAC Asn	GAC Asp	TCC Ser 315	CTC Leu	CAA Gln	ACA Thr	GGG Gly	TTC Phe 320	960
TTT Phe	GCC Ala	GCA Ala	CTA Leu	TTC Phe 325	TAC Tyr	AAA Lys	CAC His	AAA Lys	TTC Phe 330	AAC Asn	TCG Ser	TCT Ser	GGA Gly	TGC Cys 335	CCA Pro	1008
GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	AAG	TTC	GCT	CAG	GGG	TGG	1056

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Glu	Arg	Leu	Ala 340	Ser	Cys	Arg	Ser	Ile 345	Asp	Lys	Phe	Ala	Gln 350	Gly	Trp		
	CCC Pro															1	104
	TGG Trp 370															1:	152
	TGC Cys															12	200
ACG Thr	ACC Thr	GAT Asp	CGG Arg	TTT Phe 405	GGT Gly	GTC Val	CCC Pro	ACG Thr	TAT Tyr 410	AAC Asn	TGG Trp	GGG Gly	GCG Ala	AAC Asn 415	GAC Asp	12	248
TCG USer				ATT					CGG					AAC		12	296
TTC Phe																13	344
■ GGC □ Gly																13	392
	ACT Thr															14	440
GGT	TCT Ser															14	488
	CTC Leu															15	536
	ATG Met															15	584
	ACT Thr 530															16	632
	AGC Ser															16	680
	TTC Phe															17	728
	AAC Asn															17	776

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	TCC Ser															1824
	GCA Ala 610															1872
	CAA Gln										-					1920
GCC	GTG Val				CAT	-				TTC		-			TGT	1968
EAla	GCC Ala															2016
TTC Phe	TAT Tyr	GGC Gly 675	GTG Val	TGG Trp	CCG Pro	CTG Leu	CTC Leu 680	CTG Leu	CTT Leu	CTG Leu	CTG Leu	GCC Ala 685	TTA Leu	CCA Pro	CCA Pro	2064
CGA LArg				TAG	IAA											2082
(2)	INFO	ORMAT	rion	FOR	SEQ	ID N	NO: 4	18:								

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 692 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu '1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ara 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110

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Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val 155 Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro 215 T. Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala 225 230 235 240 Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Wal Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro 280 EGly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe 310 Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arq Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly 390 Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly

435 440 Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys 455 Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr 490 Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu 🖺 Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys 550 Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His 565 🖳 Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys 650 Aka Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro 680 Arg Ala Tyr Ala

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO (ix) FEATURE:

(A) NAME/KEY: CDS (B) LOCATION: 1..2430

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..2427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Met 1	AGC Ser															48
CGC CGC Arg	CGC Arg	CCA Pro	CAG Gln 20	GAC Asp	GTC Val	AAG Lys	TTC Phe	CCG Pro 25	GGC Gly	GGT Gly	GGT Gly	CAG Gln	ATC Ile 30	GTT Val	GGT Gly	96
₩ GGA ☐ Gly	GTT Val	TAC Tyr 35	CTG Leu	TTG Leu	CCG Pro	CGC Arg	AGG Arg 40	GGC Gly	CCC Pro	AGG Arg	TTG Leu	GGT Gly 45	GTG Val	CGC Arg	GCG Ala	144
ACT Thr	AGG Arg 50															192
ATC Ile																240
	CCT Pro															288
	CTG Leu															336
	CGT Arg															384
	TTC Phe 130															432
	GGC Gly															480
	GTG Val															528
	CTC Leu															576

			180			185			190		
	A GTO u Val										624
	C TCA n Ser 210	Ser									672
	G TGC y Cys 5										720
	G CTC a Leu										768
AC	A ATA										816
	C GCI r Ala										864
	G CTG n Leu 290	Phe									912
□ As □ 30	T TGC n Cys 5										960
	T ATG p Met										1008
	G CTC u Leu										1056
	G GGA p Gly										1104
	T AAG a Lys 370	Val									1152
	C CGC r Arg 5										1200
	C CTC r Leu										1248
	C GGC n Gly										1296

						TTT Phe											1344
						GAG Glu											1392
						GGT Gly 470											1440
						TGC Cys											1488
	Val	CCC Pro	GCG Ala	TCT Ser 500	CAG Gln	GTG Val	TGC Cys	GGT Gly	CCA Pro 505	GTG Val	TAT Tyr	TGC Cys	TTC Phe	ACC Thr 510	CCG Pro	AGC Ser	1536
						ACG Thr											1584
						TCG Ser											1632
Test!						TTC Phe 550											1680
Įmi:	ACC					GGC Gly											1728
						CCC											1776
						GGT Gly											1824
						AGG Arg											1872
						AGG Arg 630											1920
						TGG Trp											1968
						CTT Leu											2016

CAG Gln	ATA Ile	CTG Leu 675	CCC Pro	TGT Cys	TCC Ser	TTC Phe	ACC Thr 680	ACC Thr	CTG Leu	CCG Pro	GCC Ala	CTA Leu 685	TCC Ser	ACC Thr	GGC Gly	2064
					CAG Gln											2112
					GTC Val 710											2160
					CTG Leu											2208
ATG Met					GCT Ala											2256
GTC Val																2304
TTT Leu																2352
GGT Gly 785																2400
CTG Leu									TAGT	AA						2433

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 809 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly 65 70 75 80

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Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 150 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 170 Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr L Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp 305 Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val 385 390

Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn 440 Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn 570 ij. Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala 580 585 Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met 600 Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe 630 Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp

725

730

735

Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val 745

Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe

Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro 775

Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 790 Leu Ala Leu Pro Pro Arg Ala Tyr Ala

805

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..17
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys 10

Val

- (2) INFORMATION FOR SEQ ID NO: 52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids(B) TYPE: amino acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..22
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:
 - Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp

lai:

1 5 10 15

Ser Pro Thr Thr Ala Leu 20

- (2) INFORMATION FOR SEQ ID NO: 53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1...37
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys

1 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr 20 25 30

Pro Gly Cys Gly Lys 35

- (2) INFORMATION FOR SEQ ID NO: 54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..25
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
1 10 15

Gln Leu Arg Arg His Ile Asp Leu Leu 20 25

- (2) INFORMATION FOR SEQ ID NO: 55:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..25
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:
- Gly Gly Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr Thr 10

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Thr Ile Arg Arg His Val Asp Leu Leu 20

- (2) INFORMATION FOR SEQ ID NO: 56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:
 - Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn

Ser Thr Gly Leu

- (2) INFORMATION FOR SEQ ID NO: 57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:
 - Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro

Asn Ser Ser Ile

(2) INFORMATION FOR SEQ ID NO: 58:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Asn Val Ser

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

His Asp Ala Ile Leu His Thr Pro Gly Val Pro Cys Val Arg Glu Gly

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) LENGTH: 20 amino acids

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(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro 1 5 10 15

Thr Val Ala Thr 20

- (2) INFORMATION FOR SEQ ID NO: 62:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr 1 5 10 15

Gln Leu Arg Arg 20

- (2) INFORMATION FOR SEQ ID NO: 63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser
1 5 10 15

Ala Thr Leu Cys

- (2) INFORMATION FOR SEQ ID NO: 64:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids

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(B) TYPE: amino acid

(C) STRANDEDNESS: single

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:
        Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser
        Thr Ala Leu Asn
                        20
  (2) INFORMATION FOR SEQ ID NO: 74:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ
Leu Asn Cys Asn Glu Ser Leu Ast
1 5

Ile Tyr Gln His Lys
20

(2) INFORMATION FOR SEQ ID NO: 75:
               (B) TYPE: amino acid
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:
        Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu
                                                     10
        (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 20 amino acids
               (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: peptide
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:
        Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu
                                                     10
                                                                              15
        Arg Leu Ala Ser
                       20
  (2) INFORMATION FOR SEQ ID NO: 76:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 20 amino acids
              (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
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(ii) MOLECULE TYPE: peptide

(ii) MOLECULE TYPE: peptide

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77: Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser Gly Pro Asp Gln (2) INFORMATION FOR SEQ ID NO: 78: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

Gln Gly Trp Gly

(2) INFORMATION FOR SEQ ID NO: 77:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp

(2) INFORMATION FOR SEQ ID NO: 79:

Pro Lys Pro Cys

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

Cys Gly Pro Val (2) INFORMATION FOR SEQ ID NO: 80: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80: Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr 12) INFORMATION FOR SEQ ID NO: 81: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids <u>Ļ</u> (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81: Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr Tyr Ser Trp Gly 20 (2) INFORMATION FOR SEQ ID NO: 82: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

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(i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 20 amino acids
           (B) TYPE: amino acid(C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:
     Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe Thr Lys
     Val Cys Gly Ala
:
(i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:
     Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Val Cys Ile Gly Gly Ala
     Gly Asn Asn Thr
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Leu Asn Asn Thr

20

(2) INFORMATION FOR SEQ ID NO: 83:

(2) INFORMATION FOR SEQ ID NO: 85:

(ii) MOLECULE TYPE: peptide

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Gly Ala Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val

Ile Gly Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Arg 10 Lys His Pro (2) INFORMATION FOR SEQ ID NO: 86: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86: Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly Ser Gly Pro Trp INFORMATION FOR SEQ ID NO: 87: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87: Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp Tyr Pro Tyr Arg (2) INFORMATION FOR SEQ ID NO: 88: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

.. - ..

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp

10

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Arg Ser Glu Leu

- (2) INFORMATION FOR SEQ ID NO: 92:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr 10

Gln Trp Gln Val

5

- 12) INFORMATION FOR SEQ ID NO: 93:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu

- (2) INFORMATION FOR SEQ ID NO: 94:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

(2)	TMEO	APPARTION FOR SEQ ID NO. 93.	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: YES	
ECT		SEQUENCE DESCRIPTION: SEQ ID NO: 95: CG TGCACTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG	60
	TNEO	RMATION FOR SEQ ID NO: 96:	
以(2) 二			
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
a	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 96:	
GTI	TAACC.	AC TGCATGATG	19
(2)	INFO	RMATION FOR SEQ ID NO: 97:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 97:	

GTC	CCCATC	GA GTGCGGCTAC	20
(2)	INFO	RMATION FOR SEQ ID NO: 98:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
erraning a			
CONTROL OF THE PARTY OF T	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 98:	
<u>_</u> CG1		GG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA	45
辽 【(2)	INFO	RMATION FOR SEQ ID NO: 99:	
		SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
especially of the control of the con	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 99:	
TGC	CTCAT.	AC ACAATGGAGC TCTGGGACGA GTCGTTCGTG AC	42
(2)	INFO	RMATION FOR SEQ ID NO: 100:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 100:	

FACCCAGCAG	CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC	42
(2) INFORM	ATION FOR SEQ ID NO: 101:	
	EQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) Mo	OLECULE TYPE: DNA (genomic)	
(iii) H	YPOTHETICAL: NO	
(iii) Al	NTI-SENSE: NO	
	EQUENCE DESCRIPTION: SEQ ID NO: 101:	4.0
<pre>2) INFORM</pre>	GGGACGGAGG CCTGCCTAGC TGCGAGCGTG GG ATION FOR SEQ ID NO: 102:	42
	EQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) M	OLECULE TYPE: DNA (genomic)	
(iii) H	YPOTHETICAL: NO	
(iii) Ai	NTI-SENSE: NO	
(xi) Si	EQUENCE DESCRIPTION: SEQ ID NO: 102:	
CGTTATGTGG	CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC	48
(2) INFORM	ATION FOR SEQ ID NO: 103:	
	EQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) M(OLECULE TYPE: DNA (genomic)	
(iii) H	YPOTHETICAL: NO	
(iii) Al	NTI-SENSE: NO	
(xi) Si	EQUENCE DESCRIPTION: SEQ ID NO: 103:	
CAGGGCCGTT	CTAGGCCTCC ACTGCATCAT CATATCCCAA GC	42

(2)	INFO	RMATION FOR SEQ ID NO: 104:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 104:	
CCG	GAATG'	IA CCATGTCACG AACGAC	26
⊑(2)	INFO	RMATION FOR SEQ ID NO: 105:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
Marketine Comments of the Comm	(ii)	MOLECULE TYPE: DNA (genomic)	
e E	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 105:	
GCI	CCATT	GT GTATGAGGCA GCGG	24
(2)	INFO	RMATION FOR SEQ ID NO: 106:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 106:	
GAG	CTCCC	GC TGCTGGGTAG CGC	23
(2)	INFO	RMATION FOR SEQ ID NO: 107:	

	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
		HYPOTHETICAL: NO ANTI-SENSE: NO	
		SEQUENCE DESCRIPTION: SEQ ID NO: 107:	
CCT	CCGTC	CC CACCACGACA ATACG	25
(2)	INFO	RMATION FOR SEQ ID NO: 108:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
1.1 3	(iii)	HYPOTHETICAL: NO	
I I I	(iii)	ANTI-SENSE: NO	
		SEQUENCE DESCRIPTION: SEQ ID NO: 108:	
CTA	CCCGG	GC CACATAACGG GTCACCG	27
(2)	INFO	RMATION FOR SEQ ID NO: 109:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 109:	
GGA	GGCCT	AC AACGGCCCTG GTGG	24
(2)	INFO	RMATION FOR SEQ ID NO: 110:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs	

(ii)	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 110:	
TTCTATCG	AT TAAATAGAAT TC	22
(2) INFO	RMATION FOR SEQ ID NO: 111:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
了 【 (ii)	MOLECULE TYPE: DNA (genomic)	
	HYPOTHETICAL: NO	
	ANTI-SENSE: NO	
Section :	SEQUENCE DESCRIPTION: SEQ ID NO: 111:	
CCATACG	CT CACAGCCGAT CCC	23